



REVIEW PAPER

Hybrids and horizontal transfer: introgression allows adaptive allele discovery

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Abstract

Evolution has devised countless remarkable solutions to diverse challenges. Understanding the mechanistic basis of these solutions provides insights into how biological systems can be subtly tweaked without maladaptive consequences. The knowledge gained from illuminating these mechanisms is equally important to our understanding of fundamental evolutionary mechanisms as it is to our hopes of developing truly rational plant breeding and synthetic biology. In particular, modern population genomic approaches are proving very powerful in the detection of candidate alleles for mediating consequential adaptations that can be tested functionally. Especially striking are signals gained from contexts involving genetic transfers between populations, closely related species, or indeed between kingdoms. Here we discuss two major classes of these scenarios, adaptive introgression and horizontal gene flow, illustrating discoveries made across kingdoms.

Key words: Evolution, horizontal gene transfer, hybridisation, introgression, population genetics.

Introduction

Whether it is gradual or sudden, all organisms face change. Adaptive responses are therefore required for survival, especially in species that cannot migrate. The footprints of these responses are found throughout the genome, serving as powerful signals that tell us how populations have overcome hazards, both biotic and abiotic. The allelic changes at loci mediating adaptive changes are coming to light in rapidly increasing numbers of studies, and thanks to ongoing developments in population genomics, descriptions of these loci appear in remarkably high resolution. As a result, there is now very good evidence that diverse sources of genetic variation underlie important phenotypic changes in wild populations. Among these, introgression is emerging

as a widespread fundamental evolutionary force. The term 'introgressive hybridization', hereafter referred to as 'introgression', was introduced by [Anderson and Hubricht \(1938\)](#). They referred to the introduction of syntenic nucleotide variation by recombination from a donor species into the genome of a recipient species, usually by means of hybridization and backcrossing. We will use the terms 'introgression' and 'gene flow' as synonyms, also in cases when the units that exchange variants are populations of the same species. Largely context-dependent, introgression is influenced by an array of ecological factors that control the degree of contact between species. These biotic or abiotic factors drive selection for or against hybrid genotypes and can lead to complex patterns of genetic

Abbreviations: GIsD, genomic islands of divergence; HGT, horizontal gene transfer; PaIS, parapatrically isolated species; TEs, transposable elements.

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admixture (Hand *et al.*, 2015). This selection has important consequences: adaptive introgression commonly results in local adaptation to particular geographically distributed conditions and/or speciation (Dobzhansky, 1937; Mayr 1942; Coyne and Orr, 2004).

Here we discuss the three dominant sources of genetic variation and their relative contributions to adaptation. We show how genomic approaches are revolutionizing the discovery of adaptive alleles involved in natural solutions to diverse challenges. We highlight how the studies of introgression and speciation are linked, with speciation commonly occurring in the face of gene flow. This can create hallmark genomic architectures that facilitate the discovery of adaptive alleles, which can lead to 'genomic islands of divergence' that are resistant to gene flow. We argue that the novel merger of hybrid zone analysis and whole genome population resequencing is a powerful novel tool to detect variants mediating diverse adaptations. We provide an overview of important approaches taken to identify introgressed alleles that can be applied by researchers working on virtually any system and that have the potential to unambiguously identify strong candidates for adaptively introgressed alleles. Finally, we highlight horizontal gene transfer (HGT), a special case of adaptive introgression between species with established reproductive boundaries.

Maladaptive introgression

Before discussing introgression generally and adaptive introgression in particular, it is important to note that not all introgression is adaptive; indeed, introgression is a powerful force and can be strongly disruptive, particularly as the result of human activity. Introgression even has the potential to hinder conservation attempts (Allendorf *et al.*, 2001; Edmands, 2007). Due to a shortage of conspecific mates (Vaz Pinto *et al.*, 2016), introgression may drive rare species to extinction by genetic swamping (Wolf *et al.*, 2001; Gómez *et al.*, 2015; Todesco *et al.*, 2016). Conservation attempts based on the translocation of species to reserves outside native ranges can result in introgression and inadvertent admixture that damages the biodiversity of the protected species (e.g. antelope; van Wyk *et al.*, 2017). In addition, introgression between crops or domesticated animals and wild relatives can alter fitness-related traits, such as disease resistance and growth, although every case is unique. Recent examples include introgression from domesticated dogs into wolves (Anderson *et al.*, 2009), between farmed and native salmonids (Glover *et al.*, 2013; Ozerov *et al.*, 2016; Karlsson *et al.*, 2016), from wild pigs into domesticated pigs (Ai *et al.*, 2015), from wildcats into domesticated cats (Ottoni *et al.*, 2017), between maize and teosinte (Hufford *et al.*, 2012; Hufford *et al.*, 2013), from domesticated rice into wild rice (Wang *et al.*, 2017), and between genetically modified plants and their wild relatives (den Nijs *et al.*, 2004). Introgression between native and introduced, often invasive, species has also been reported, with examples including mussels (Saarman and Pogson, 2015), salamander (Fitzpatrick *et al.*, 2010; Wilcox *et al.*, 2015), trout (Hohenlohe *et al.*, 2013;

Muhlfeld *et al.*, 2014; Kovach *et al.*, 2015; Kovach *et al.*, 2016) and *Ulmus* trees (Zalapa *et al.*, 2009). Genomes may be resistant to the introgression of invading alleles when selection favours the native allele, as shown in, for example, trout (Kovach *et al.*, 2015; Kovach *et al.*, 2016) and *Arabidopsis thaliana* (Lee *et al.*, 2017). Interestingly, adaptive introgression can also occur differentially from one subgenome of an allopolyploid, for example from wheat into *Aegilops* (Parisod *et al.*, 2013).

Introgression as an engine of adaptive genetic variation

There are three primary sources of genetic variation: (1) pre-existing or 'standing' variants, which are the variants already present in a population, (2) new mutations, and (3) introgression (reviewed in Olson-Manning *et al.*, 2012; Hedrick, 2013). Despite introgression traditionally being seen as maladaptive, there is growing literature demonstrating the widespread occurrence of adaptive introgression (reviewed in Mallet *et al.*, 2016). Introgression is implicated to be a powerful adaptive force in a wide array of taxa, including, for example, the malaria transmitting mosquito *Anopheles* (Clarkson *et al.*, 2014; Fontaine *et al.*, 2015), *Heliconius* butterflies (Zhang *et al.*, 2016), mice (Song *et al.*, 2011), humans (Racimo *et al.*, 2017), *Arabidopsis* (Arnold *et al.*, 2016), sunflowers (Whitney *et al.*, 2015), and monkeyflowers (Stankowski and Streisfeld, 2015). However, the relative importance of introgression, *de novo* mutation, and standing variation is far from resolved. Barton (2001) concluded that adaptive variation engendered by mutation is likely to exceed that brought about by introgression. This is all the more likely if the effective population sizes are large because the probability of a favourable mutation is a function of effective population size. For example, many pests and weeds have tremendous effective population sizes and there is strong evidence that cases of escape from chemical insecticides and herbicides have originated many times from independent novel mutations, for example in *Drosophila* (Karasov *et al.*, 2010) and in weeds (Délye *et al.*, 2013). However this is not always the case, for example *Anopheles* traits enhancing vectorial capacity, including the knockdown resistance mediated by a specific single nucleotide polymorphism, were transferred between two hybridizing species (Weill *et al.*, 2000).

Anderson (1949) suggested that introgressed variation should have a higher initial frequency than new adaptive mutations and a lower initial frequency than standing variation. But if introgression is recurrent and results in fit progeny, early frequencies could be much higher, exceeding the adaptive potential of standing variation. Further, the impact of single introgressed variants on the genome can be sizable, typically causing multiple changes within a gene and at times affecting several gene-coding loci. Striking examples involve the transfer of entire complex adaptations via cassettes of multiple linked mutations, such as those in loci that control wing colour patterns for both mimicry and mate recognition in *Heliconius* butterflies (The *Heliconius* Genome Consortium, 2012). Such an

advantage can also be found in some cases of adaptive standing variation (Bastide *et al.*, 2016) and occasionally for *de novo* adaptive mutations (Karasov *et al.*, 2010). In addition, introgressed alleles feature the benefit that they are likely to have been pre-tested by selection in a usually closely related donor species and would therefore be less likely to be deleterious than random mutations (Hedrick, 2013). Indeed, introgressed variants that initially have no strong advantage or disadvantage can accumulate in the genome as cryptic variation, which then serves as the raw material for selection when conditions change (reviewed in Paaby and Rockman, 2014).

The ability to introgress is dependent on the degree of divergence, as introgression between more divergent species is usually impeded by pre- and post-zygotic reproductive barriers. It has recently been suggested that polyploidy can occasionally rescue introgression between otherwise reproductively isolated species. For example, polyploidization re-established normal endosperm cellularization and enabled unidirectional interplodid introgression and bidirectional introgression between tetraploids of *Arabidopsis arenosa* and *Arabidopsis lyrata* (Lafon-Placette *et al.*, 2017). A case of introgression between the autotetraploid cytotypes of these species reports the exchange of candidate alleles for mediating adaptation to highly challenging serpentine soils (Arnold *et al.*, 2016). Interplodid introgression is generally assumed to be unidirectional, from diploid to polyploid (Stebbins, 1971), although there is evidence that it can also occur in the reverse direction (Ramsey and Schemske, 1998). There have been very few genomic studies on interplodid introgression and nearly all reports detail gene flow from diploids to tetraploids, for example in *Betulus* (Zohren *et al.*, 2016). Another study in *Miscanthus* favoured the same unidirectionality of gene flow, although there was some evidence for occasional gene flow from polyploids to diploids (Clark *et al.*, 2015). Due to the scarcity of genomic studies one is left with literature based on only handfuls of molecular markers, the vast majority of which support gene flow from diploids to polyploids, such as in *Senecio* (Kim *et al.*, 2008; Chapman and Abbott, 2010), *Epidendrum* (Pinheiro *et al.*, 2010), and *Capsella* (Han *et al.*, 2015). Except for Kim *et al.* (2008) and Chapman and Abbott (2010) who found evidence of introgression of fitness-related genes, it is unclear whether interplodid introgression frequently leads to the transfer of adaptive alleles.

Hybridization, particularly in cases where hybridization leads to allopolyploidy, and introgression can also introduce variation at the structural level leading to genome rearrangements and novel gene regulatory pathways through the reactivation of dormant transposable elements (TEs) (reviewed in Fontdevila, 2005). For instance, introgression between cultivated and wild rice led to changes in transcription levels and DNA methylation patterns in TE-rich genomic regions (Liu *et al.*, 2004). Introgression between bread wheat and tall wheatgrass led to various genetic and epigenetic changes, including deletions, differences in gene expression and TE reactivation (Liu *et al.*, 2015). Similar changes have been identified in introgression lines between cauliflower (*Brassica oleracea*) and black mustard (*Brassica nigra*), creating variation that might prove useful for trait selection in breeding (Wang *et al.*, 2016).

Introgression aids adaptive allele discovery in the genomic era

The widespread occurrence of introgression suggests promise in mining for adaptive alleles in natural populations that have overcome identifiable biotic or abiotic challenges. In parallel, there is a growing interest in how knowledge obtained from more broadly observing natural solutions devised by evolution might inform breeding efforts. Mining for introgressed alleles between natural populations that are native to contrasting environments offers the possibility to identify candidate alleles that mediate definable adaptations. Indeed, it has been long recognized that especially where fitness-related traits and genotypes show clinal variation, gene-environment associations can provide a window on the mechanisms of natural selection (Endler, 1977). Such information is virtually impossible to discover with experimental crosses, although evolve and resequence experiments can be informative (reviewed in Long *et al.*, 2015). However, mining for adaptive alleles in natural populations with population genomics, namely ‘reverse ecology’ (Li *et al.*, 2008), complements and in many ways surpasses candidate gene-based approaches. By providing a genome-wide view of the divergence landscape, population genomic studies can overcome key limitations of candidate-based approaches; for instance, they can detect polygenic adaptation provided markers are dense, that is to say genome resequencing as opposed to restriction site associated DNA sequencing. Such mining for co-evolved alleles involved in a trait is facilitated if frequencies of these alleles follow a clinal pattern in a hybrid zone that may coincide with an environmental gradient.

Genome-wide data from populations that are characterized by a history of extensive gene flow can provide detailed insights into the genetic basis of adaptive divergence. Usually in such cases only a few loci under selection rise above the neutral background that is homogenized by gene flow. Here we focus on these population genomic studies, because they can leverage sufficient resolution and statistical power to detect non-random patterns of introgression. We note, however, that crucial insights into the evolutionary role of adaptive introgression were made before the advent of high-throughput sequencing and population genomic datasets (reviewed in Arnold and Martin, 2009). Indeed, population genomics and comparative phylogenomics are young fields and sometimes issues with data quality or analytical rigor can raise concerns that render results ambiguous (Brower, 2013; Wen *et al.*, 2016). Nevertheless, with well-designed sampling and increasingly sophisticated analysis, evidence of genomic heterogeneity in patterns of gene flow has been accumulating at all levels from weakly (Arnold *et al.*, 2016) to highly differentiated (Pardo-Diaz *et al.*, 2012) species. Understanding these population- and genome-wide patterns of introgression in species with diverse adaptations has broad potential to contribute to our understanding of the fundamental mechanisms of adaptation.

The genomic architecture of introgression

The study of introgression in natural populations is deeply connected with the study of speciation. It is increasingly recognized that speciation frequently occurs in the face of gene flow;

either through continual gene flow or phases of secondary contact in species that have already established partial reproductive isolation, hereafter referred to as parapatrically isolated species (PaIS) (Nosil, 2008; Feder *et al.*, 2012; Abbott *et al.*, 2013; Harrison and Larson, 2014; Mallet *et al.*, 2016; Shapiro *et al.*, 2016; Arnold, 2016). One iconic example is the sunflower *Helianthus annuus* subsp. *texanus*, which originated as a result of introgression and shows different adaptations compared with its parents, mainly abiotic tolerance traits (Whitney *et al.*, 2010; Whitney *et al.*, 2015). It may be difficult to discriminate ongoing divergence from secondary contact in PaIS (Endler, 1977; Harrison, 2012; Gompert and Buerkle, 2016), especially in cases where species have recently diverged. Both scenarios of introgression offer potential insights into the mechanisms of adaptive introgression, although major findings have been made in cases of secondary contact (Table 1), as speciation-with-gene-flow studies usually aim to identify loci involved in the establishment and maintenance of reproductive isolation and not loci involved in local adaptation. Strong evidence for secondary contact in major systems that allow the study of adaptive introgression comes from clear estimates of the time of secondary contact as well as the delineation of clearly defined hybrid zones. Both the time of species divergence and secondary contact are relatively young in these systems (Table 1). Except for the hybridization between *Heliconius erato* and *H. melpomene* (Martin *et al.*, 2013; Kozak *et al.*, 2015) and *Saccharomyces cerevisiae* and *S. uvarum* (Kellis *et al.*, 2003), all other study systems show divergence times for the introgressing species of usually much less than 2 mya and times of secondary contact between a few hundred and few thousand years before the present time.

Introgression between divergent populations or closely related species does not generally homogenize divergence levels across the entire genome (Turner *et al.*, 2005; Coleman *et al.*, 2006; Harr, 2006; Michel *et al.*, 2010; Hohenlohe *et al.*, 2012; Via, 2012; Renaut *et al.*, 2013; Malinsky *et al.*, 2015; Marques *et al.*, 2016; reviewed in Wolf and Ellegren, 2017). Genomic islands of divergence (GIsD), also known as genomic islands of speciation, manifest as regions of elevated divergence in a 'sea' of neutral, non-differentiated background that has been homogenized by a history of gene flow. These GIsD are typically attributed to loci under divergent selection contributing to adaptation to the local environment or the establishment of reproductive isolation relatively independent of the external environment (Wu and Ting, 2004; Orr *et al.*, 2004; Rieseberg and Blackman, 2010; Nosil and Schluter, 2011). One example is the adaptation to different foraging behaviours in Darwin's finches, which might have largely been driven by the *ALX1* gene that encodes a transcription factor affecting craniofacial development. Variation in this gene is strongly associated with beak shape diversity across Darwin's finches and the medium ground finch (Lamichhane *et al.*, 2015). GIsD have been reported in many cases of recent species divergence with ongoing gene flow (Martin *et al.*, 2013; Jónsson *et al.*, 2014; Supple *et al.*, 2015; Rougeux *et al.*, 2016; Royer *et al.*, 2016; Morales *et al.*, 2017; Kumar *et al.*, 2017). The region of divergence typically extends away from the selected locus due to physical linkage, allowing neutral polymorphisms to

hitchhike along with a selected polymorphism, namely divergence hitchhiking, and become part of the GIsD. In many cases, this can obscure signals of selection and lead to ambiguity over the exact genetic loci under selection. It is therefore advisable to incorporate linked selection as a null model for the identification of genomic regions exhibiting pronounced differentiation (Burri *et al.*, 2015).

Low recombination rates in some genomic regions can also create GIsD. Regions of suppressed recombination are frequently pericentromeric and often involve structural changes such as inversions that can physically block recombination. They are thought to sometimes play a role in adaptive genomic divergence (Rieseberg, 2001; Noor *et al.*, 2001; Feder and Nosil, 2009), for example in the case of the 2L inversion divergence island, which was introgressed from *Anopheles gambiae* into *A. coluzzii* and harbours a suite of insecticide-resistance alleles (Lee *et al.*, 2013a; Norris *et al.*, 2015). However, it is questionable if most regions of very low recombination contain loci under divergent selection or whether they were simply established due to the stochastic effects of genome structure and genetic drift (Turner and Hahn, 2010). If the amount of gene flow is very low, for example due to geographic isolation, then large blocks of pronounced genomic differentiation may arise from genetic drift. This could be further accentuated by variable mutation rates and low recombination rates (Noor and Bennett, 2009; White *et al.*, 2010; Cruickshank and Hahn, 2014).

Traits impacted by adaptive introgression

The traits impacted by introgression are as diverse as the organisms that have been studied (Table 1). In plants, for example, a broad array of abiotic tolerance traits have been affected, for example ion homeostasis and drought adaptations (*Arabidopsis arenosa*, Arnold *et al.*, 2016; sunflowers, Whitney *et al.*, 2015), but also traits that control biotic interactions between plants and herbivores (sunflowers, Whitney *et al.*, 2015) or pollinators (*Senecio*, *RAY1* and *RAY2* genes, Kim *et al.*, 2008), and others (poplars, *PRR5* and *COMT1* genes, Suarez-Gonzalez *et al.*, 2016). In animals, clear examples that include traits influenced by adaptive introgression include insecticide resistance in *Anopheles*, the single nucleotide polymorphism L1014F in the gene *kdr* (Fontaine *et al.*, 2015; Norris *et al.*, 2015) and rodenticide resistance in mice, the *vkorc1* gene (Song *et al.*, 2011). Other introgressed alleles of potentially adaptive value stem from the actin gene *mac-1* in mussels (Fraïsse *et al.*, 2014), several loci that control wing colour patterns for both mimicry and mate recognition, amongst them the *optix* locus in *Heliconius* butterflies (Nadeau *et al.*, 2014; Zhang *et al.*, 2016), the beak shape-associated locus *ALX1* in Darwin's finches (Lamichhane *et al.*, 2015), variants that control lipid metabolism, pigmentation and innate immunity in humans (Racimo *et al.*, 2017), but also loci of so far uncharacterized adaptive value in *Drosophila* (Garrigan *et al.*, 2012; Brand *et al.*, 2013) and mice (Staubach *et al.*, 2012). An interesting case of introgression between *Drosophila* species was reported to be

Table 1. Important systems for the study of adaptive introgression in natural populations. Studies leveraging genome-wide high-throughput sequencing data were selected and employed methods of demographic inference and genome architecture of introgression are listed, which are described in Table 2. Especially in intensely studied systems, i.e., *Drosophila*, *Heliconius* butterflies, humans and yeast, we restricted the number of case studies to the most recent and/or in our opinion highly interesting ones

Hybrid partners	Genomic data types	Methods applied	Adaptive traits or genes influenced	Start of divergence of the hybridizing taxa	Estimated time of secondary contact	Presence of hybrid zone(s)
Arabidopsis						
Between <i>Arabidopsis arenosa</i> and <i>A. lyrata</i> (Schmickl and Koch, 2011; Arnold <i>et al.</i> , 2016)	Whole genome sequencing (Arnold <i>et al.</i> , 2016)	Fastsimcoal2, f_D statistic, HybridCheck; genome scan	Genes controlling specific ion homeostasis-related and drought adaptation traits (Arnold <i>et al.</i> , 2016)	~1.63 mya (Hohmann <i>et al.</i> , 2015)		Eastern Austrian Forealps (Schmickl and Koch, 2011)
Sunflowers						
From <i>Helianthus debilis</i> subsp. <i>cucumerifolius</i> into <i>H. annuus</i> subsp. <i>annuus</i> (Whitney <i>et al.</i> , 2015)	SNP dataset (QTL mapping)		Primarily abiotic tolerance traits allowing rapid growth and reproduction before summer heat and drought, but also traits affecting herbivore resistance	Divergence between the ancestors of <i>H. debilis</i> and <i>H. annuus</i> ~2 mya (Renaut <i>et al.</i> , 2013)	Maximum ~18,000 ya (Scascitelli <i>et al.</i> , 2010)	South-central USA
Senecio						
From diploid <i>Senecio squaidus</i> into tetraploid <i>S. vulgaris</i> (Kim <i>et al.</i> , 2008)	[No large genome-wide dataset] Sanger sequencing, RNA in situ hybridization		Genes RAY1 and RAY2 that control ray florets in radiate flower heads, which effects attractiveness to pollinators and outcrossing rate	<i>S. squaidus</i> is a homoploid hybrid with an origin less than ~150,000 ya (Filatov <i>et al.</i> , 2016)	Maximum ~300 ya (<i>S. squaidus</i> was introduced to the Oxford Botanic Garden around 300 ya)	United Kingdom
Poplars						
From <i>Populus balsamifera</i> into <i>P. trichocarpa</i> (Suarez-Gonzalez <i>et al.</i> , 2016)	Whole genome sequencing, RNaseq	Genome scan	Numerous genes, particularly in a telomeric region (<i>PRR5</i> and <i>COMT1</i>); related to response to far red light, RNA processing and ATPase activity	~76,000 ya (Levsen <i>et al.</i> , 2012)		Northwestern North America
Mussels						
From <i>Mytilus edulis</i> into <i>M. galloprovincialis</i> (Fraissee <i>et al.</i> , 2014; Fraissee <i>et al.</i> , 2016)	AFLP and few other markers, Sanger sequencing (Fraissee <i>et al.</i> , 2014); target enrichment (Fraissee <i>et al.</i> , 2016)	Genome scan	Actin gene <i>mac-1</i> (Fraissee <i>et al.</i> , 2014; but not Fraissee <i>et al.</i> , 2016)	~2.5 mya (Roux <i>et al.</i> , 2014)	~0.7 mya (Roux <i>et al.</i> , 2014)	In Europe from the Mediterranean Sea to the North Sea
Drosophila						
From <i>Drosophila simulans</i> into <i>D. sechellia</i> (Garrigan <i>et al.</i> , 2012; Brand <i>et al.</i> , 2013)	whole genome sequencing; Sanger sequencing of the candidate region identified by Garrigan <i>et al.</i> , 2012	Genome scan (Garrigan <i>et al.</i> , 2012)	A 15 kb region (Garrigan <i>et al.</i> , 2012) – the target of selection appears to be a regulatory sequence; evidence for a trans-specific selective sweep (Brand <i>et al.</i> , 2013), i.e., the 15 kb region harbours a polymorphism that is adaptive in both species	~200,000–300,000 ya (Garrigan <i>et al.</i> , 2012)	2,600–18,600 ya	Seychelles

Table 1. Continued

Hybrid partners	Genomic data types	Methods applied	Adaptive traits or genes influenced	Start of divergence of the hybridizing taxa	Estimated time of secondary contact	Presence of hybrid zone(s)
From <i>D. yakuba</i> into <i>D. santomea</i> (Lopart et al., 2014; Beck et al., 2015)	Lopart et al., 2014; Sanger sequencing and high-throughput sequencing of the mitochondrial genome; Beck et al., 2015; Sanger sequencing		Potential cytonuclear co-introgression of genes involved in the oxidative phosphorylation pathway; strong signal of introgression in the three nuclear genes composing subunit V of the cytochrome c oxidase complex (Beck et al., 2015)	~400,000 ya (Lopart et al., 2002)	~14,000 ya (complete replacement of the mitochondrial genome) and ~2,500 years ago (Lopart et al., 2014)	São Tomé (invasion by <i>D. yakuba</i>)
Anopheles Between <i>Anopheles arabiensis</i> and the ancestor of <i>A. gambiae</i> and <i>A. coluzzii</i> (Fontaine et al., 2015)	Whole genome sequencing	<i>D</i> and <i>D_{FOL}</i> statistics, window-based gene tree distribution across chromosomes	Insecticide-resistance alleles might have introgressed into <i>A. arabiensis</i> with the 2La inversion introgressed from the ancestor of <i>A. gambiae</i> and <i>A. coluzzii</i>	Divergence between <i>A. gambiae</i> and <i>A. coluzzii</i> from its ancestor ~2 mya	~0.5 mya	Central Africa
From <i>A. gambiae</i> into <i>A. coluzzii</i> (Norris et al., 2015)	SNP genotyping, whole genome sequencing		Traits enhancing vectorial capacity: <i>A. coluzzii</i> inherited the entire <i>A. gambiae</i> -associated 2L divergence island including the knockdown resistance SNP L1014F in the <i>kdr</i> gene (L1014F has been present in <i>A. gambiae</i> populations for at least 20 years)	Periods of isolation interrupted by hybridization; recent introgression reported in 2002 and 2006 (Lee et al., 2013b)		Selinkenyi, Mali
Heliconius butterflies Other studies that focused on speciation with ongoing gene flow and adaptive introgression: e.g. Pardo-Diaz et al., 2012; The Heliconius Genome Consortium, 2012; Nadeau et al., 2013; Krontorst et al., 2013; Martin et al., 2013)	RAD-seq	Structure; genome scan	Loci that control wing color patterns (for both mimicry and mate recognition); the aim of this study was to identify novel loci underlying phenotypic variation by means of association mapping in hybrid zones	~11.8 mya (Kozak et al., 2015)	Several time points post speciation (Martin et al., 2013)	Parallel zones in the Andes

Table 1. Continued

Hybrid partners	Genomic data types	Methods applied	Adaptive traits or genes influenced	Start of divergence of the hybridizing taxa	Estimated time of secondary contact	Presence of hybrid zone(s)
Between <i>H. beschkei</i> , <i>H. numata</i> and <i>H. numata</i> subsp. <i>nanna</i> (Zhang <i>et al.</i> , 2016)	Whole genome sequencing	D and f_D statistics	Genomic region upstream of the gene <i>optix</i> (known to control red wing patterning) and 39 additional genomic regions	Divergence between <i>H. beschkei</i> and <i>H. numata</i> ~1.93 mya		East-central South America
Darwin's finches Species from different Galápagos islands (Lamichhaney <i>et al.</i> , 2015)	Whole genome sequencing	PSMC, NeighborNet, D statistic; genome scan	ALX1 gene encodes a transcription factor controlling craniofacial development, in particular beak shape	~0.5 mya	Several time points post speciation	Galápagos islands
Mice From <i>Mus spretus</i> into <i>M. musculus</i> subsp. <i>domesticus</i> (Song <i>et al.</i> , 2011)	[No large genome-wide dataset] Sanger sequencing		>10 Mb region including the molecular target of anticoagulants <i>vkorc1</i> ; <i>M. spretus</i> -specific alleles can cause resistance to rodenticides	~1.5–3 mya		Africa and Europe
Between <i>M. musculus</i> subsp. <i>domesticus</i> and <i>M. musculus</i> subsp. <i>musculus</i> (Staubach <i>et al.</i> , 2012)	SNP genotyping	Genome scan	No general pattern of types of genes subject to introgression	300,000–500,000 ya (Guénét and Bonhomme, 2003)	Maximum ~3,000 ya (Cucchi <i>et al.</i> , 2005)	Eastern and southern Germany, western Czech Republic
Humans Other studies identified genomic regions with evidence of adaptive introgression between archaic and modern humans (from Neanderthals into modern humans: e.g., Vernot and Akey, 2014; Sankararaman <i>et al.</i> , 2014 / from Denisovans into Tibetans: e.g., Jeong <i>et al.</i> , 2014; Huerta-Sánchez <i>et al.</i> , 2014)						
From Neanderthals and Denisovans into modern humans (Racimo <i>et al.</i> , 2017)	Whole genome sequencing; reevaluation of published data	D and f_D statistics, F_D , U and Q95 statistics, Haplostrips	Lipid metabolism, pigmentation and innate immunity	Divergence between the Neanderthal/Denisovan lineage and modern humans 170,000–700,000 ya (Meyer <i>et al.</i> , 2012)	Between Neanderthals and modern humans 47,000–65,000 ya (Sankararaman <i>et al.</i> , 2012)	Eurasia

Table 1. Continued

Hybrid partners	Genomic data types	Methods applied	Adaptive traits or genes influenced	Start of divergence of the hybridizing taxa	Estimated time of secondary contact	Presence of hybrid zone(s)
Yeast Between <i>Saccharomyces cerevisiae</i> and <i>S. uvarum</i> (Dunn et al., 2013)	Whole genome sequencing, colony-PCR and qRT-PCR		MEP2 fusion gene encodes for a high-affinity ammonium permease, which may be adaptive under nitrogen-poor environments with ammonium as only nitrogen source	~20 mya (Kellis et al., 2003)	de novo creation of hybrid followed by continuous ammonium limitation	Experimental populations
<i>Albugo candida</i> Between the ancestors of three races; an adaptive radiation in progress (McMullan et al., 2015)	Whole genome sequencing, RNAseq	HybridCheck	Effector alleles that may result in a fitness advantage on most potential hosts, enabling host jumps		Multiple time points; oldest event ~200,000 ya, most recent event ~2,200 ya	Infection with virulent <i>A. candida</i> suppresses host immunity enabling co-colonization by otherwise non-virulent races

trans-specific, meaning that the introgressed 15 kb region harbours a mutation that appears adaptive in both species despite their different genomic backgrounds and ecological requirements (Brand et al., 2013). In addition, cytonuclear co-introgression has been shown for some *Drosophila* species (Beck et al., 2015). In the fungal genus *Saccharomyces* experimental hybridisation followed by ammonium limitation resulted in the origin of an interspecific MEP2 fusion gene, which encodes for a high affinity ammonium permease that may be adaptive under nitrogen-poor environments with ammonium as the only nitrogen source (Dunn et al., 2013).

Adaptive allele mining in hybrid zones

In secondary contact scenarios, PaIS come into contact following a period of reproductive isolation. This process is often induced by geographic and environmental factors, such as habitat shifts due to climate changes, for example oscillations during Pleistocene and Anthropocene, or catastrophic human-mediated events such as fires, flooding, road construction or introduction of alien species (Crispo et al., 2011). Such secondary contact between divergent but interfertile populations frequently results in hybrid zones where the otherwise geographically distinct distribution ranges of the two species overlap, permitting the production of offspring of mixed ancestry (Barton and Hewitt, 1985; Barton and Hewitt, 1989; Harrison, 1990). In the fungus-like pathogen *Albugo candida* a spectacular example of adaptive introgression after secondary contact has recently been reported, in which infection of a host with virulent *A. candida* suppresses host immunity enabling co-colonization by otherwise non-virulent races (McMullan et al., 2015). This creates hybrid zones allowing sexual reproduction and gene flow between isolated races; effector alleles are transferred that exhibit a fitness advantage on many potential hosts, facilitating host jumps. Then once a new hybrid race has established, it rapidly reproduces asexually without continued exchange with other races.

Hybrid zones represent natural laboratories (Hewitt, 1988) for the study of introgression dynamics as well as their evolutionary significance. They offer venues to observe allele flow between partly isolated populations and allow hybrid fitness to be estimated in nature. As described above, alleles under divergent selection are relatively inhibited from introgressing between populations. This barrier to the exchange of certain alleles generates an allele frequency gradient, or cline, across the hybrid zone, which partly blocks the homogenization of the hybridizing populations. Such a cline might be detected as a phenotypic transition from one parental species to the other, which should coincide with the underlying allelic cline. Hybrid zones can be understood as natural mapping experiments to determine the alleles responsible for complex traits that differentiate parental populations (Buerkle and Lexer, 2008; Crawford and Nielsen, 2013). Over generations, recombination breaks down linkage, allowing alleles at discrete loci to be associated with phenotypes and environmental variables (Crawford and Nielsen, 2013). This is especially clear in large hybrid populations with varying levels of admixture that are established along environmental gradients, such as in spruce

Table 2. Useful population genomic and phylogenomic approaches to detect and interpret introgression events

Analysis Type	Software	Description	References
Demographic inference	Population structure		
	adeigenet	Evaluation of population clustering using principal component and discriminant analysis	Jombart, 2008; Jombart <i>et al.</i> , 2010
	STRUCTURE; fastSTRUCTURE; fineSTRUCTURE; ADMIXTURE; SpaceMix	Estimation of (fine-scale) population structure, taking admixture into account	Pritchard <i>et al.</i> , 2000; Hubisz <i>et al.</i> , 2009; Raj <i>et al.</i> , 2014; Lawson <i>et al.</i> , 2012; Alexander <i>et al.</i> , 2009; Bradburd <i>et al.</i> , 2016
	Demographic history		
	IM; IMa2	Fitting an isolation with migration model to haplotype data from two populations (IM) or up to ten populations (IMa2)	Hey and Nielsen, 2007; Hey J. 2010a; Hey J. 2010b
	dadi (diffusion approximations for demographic inference)	Inference of the demographic history of multiple populations from SNP frequency data	Gutenkunst <i>et al.</i> , 2009
	PSMC (pairwise sequentially Markovian coalescent model); MSMC (multiple sequentially Markovian coalescent model)	Inference of fluctuations in effective population size over time from a single genome sequence (PSMC) or multiple genome sequences (MSMC)	Li and Durbin, 2011; Schiffels and Durbin, 2014
	simcoal2; fastsimcoal2	Inference of parameter values, such as population split times and migration rates, and testing of hypotheses to compare to alternative, neutral demographic scenarios	Laval and Excoffier, 2004; Excoffier <i>et al.</i> , 2013
	Rarecoal	Inference of population history and fine-scale ancestry from rare variants	Schiffels <i>et al.</i> , 2016
	Network and tree methods		
	NeighbourNet (SplitsTree4)	Visualization of reticulate relationships in the form of splits networks	Huson and Bryant, 2006
	TreeMix	Inference of patterns of population splits and admixture	Pickrell and Pritchard, 2012
	Phylo-Net	Coalescent-based species tree and evolutionary network method; testing the number of introgression events	Than <i>et al.</i> , 2008
Genomic architecture of introgression	Introgression detection		
	D statistic; f statistic	Detection of SNP window-based or genome-wide evidence of shared alleles (ABBA-BABA test) in a four-taxon case	Comparison of two genomes: Green <i>et al.</i> , 2010; Durand <i>et al.</i> , 2011 / comparison of two populations: Kronforst <i>et al.</i> , 2013; Smith and Kronforst, 2013
	D_{FOIL} statistic	D statistic for a symmetric five-taxon phylogeny; determination of the directionality of introgression	Pease and Hahn, 2015
	f_D statistic	Refinement of the f statistic (Green <i>et al.</i> , 2010) by being less sensitive to differences in diversity along the genome	Martin <i>et al.</i> , 2015
	R_D , U , $Q95$ statistics	Identification of genomic windows that are likely to have undergone adaptive introgression	Racimo <i>et al.</i> , 2017
	Methods with additional visualization aspect		
	HybridCheck	Detection of introgressed genomic blocks and visualization of the heterogeneous, mosaic-like genome structure; dating of introgressed blocks	Ward and van Oosterhout, 2016
	Haplostrips	Plot of haplotype structure at candidate regions for adaptive introgression	Marnetto <i>et al.</i> , in prep. (cited in Racimo <i>et al.</i> , 2017)
	Twisst	Topology weighting of SNP window-based trees across the genome	Martin and Van Belleghem, 2017

(Hamilton *et al.*, 2013; Hamilton *et al.*, 2015). Substantial levels of clinal variation and allele-environment associations with climatic variables such as temperature and precipitation were found in hybrid zones of Sitka, white, and Engelmann spruce (Hamilton *et al.*, 2015), which suggests that species integrity is maintained through exogenous selection in parental habitats and that hybridisation might facilitate fine-scale adaptation of the species along environmental gradients.

However, genotype-phenotype-environment associations along clines have rarely been addressed using dense genome-wide markers. Highlights include work in mice (Turner and Harr, 2014; Pallares *et al.*, 2014; Pallares *et al.*, 2016), for which genes involved in craniofacial shape variation were found that act in a polygenic manner (Pallares *et al.*, 2016). The *Heliconius* and *Helianthus* systems are other examples of association mapping across hybrid zones, although

Helianthus showed spurious associations in early generation hybrids due to linkage disequilibrium (Rieseberg and Buerkle, 2002). *Heliconius* in contrast is a relatively old hybrid zone and close to linkage equilibrium, with phenotypic variation largely controlled by major effect loci, for which smaller sample sizes are sufficient (Nadeau *et al.*, 2014). With emerging probabilistic frameworks to infer allele frequencies in low coverage sequencing data it should be possible in the future to also address minor effect loci, for which larger sample sizes are required, even in polyploids (Blischak *et al.*, 2017).

Selective landscapes vary widely in different types of hybrid zones. If selection acts on genotypes of mixed ancestry independent of spatial variation in selection pressures, the hybrid zone can be considered a 'tension zone' (Barton and Hewitt, 1985; Barton and Hewitt, 1989). In a tension zone selection is usually endogenous, for example the hybrid zone between two *Senecio* species on Mount Etna (Brennan *et al.*, 2009), with occasional exceptions such as exogenous frequency-dependent selection by predatory birds in *Heliconius* butterflies (Mallet *et al.*, 1990). Alternatively, Endler (1977) postulated spatially varying exogenous selection along a geographic-environmental gradient. According to another model, the bounded hybrid superiority model (Moore, 1977), selection in intermediate habitats can favour individuals of mixed ancestry, which seems to be the case for the hybrid zone between Sitka and white spruce (Hamilton *et al.*, 2013). In mosaic hybrid zones, parental populations are distributed in a patchy landscape. Examples of such hybrid zones are frequently found in parasites that rely on patchily distributed hosts, for example in *Albugo candida* (McMullan *et al.*, 2015), but also in non-parasitic species such as mussels (Fraisé *et al.*, 2014), which may reflect a common scenario of complex environmental mosaics in nature (Harrison, 1986). In a tension zone, with endogenous selection on the hybrids, the hybrid zone can move freely if there are asymmetries in selection, dispersal, or population density and will finally arrest at a geographic barrier or in an area of low population density (Hewitt, 1975; Barton, 1979; Barton and Hewitt, 1985). Hybrid zones might move in response to climate change or co-varying environmental factors (Taylor *et al.*, 2015).

Population genomic approaches to infer introgression in natural populations

A convergence of recent work on new methods of refined demographic inference and methods to describe the genomic architecture of introgression have great potential for the discovery of introgressed alleles (Table 2). Demographic inference methods evaluate population structure. They provide a good estimate of admixture between populations. They estimate fine-scale demographic histories, such as population history, including fluctuations in effective population size over evolutionary time, partly based on rare polymorphisms, or they infer parameter values, such as population split times and migration rates, and test hypotheses for comparison with alternative demographic scenarios. The genomic architecture of introgression is observed using metrics that determine the

level of allele sharing and linkage disequilibrium, along with visualization methods, including topology weighting of trees across the genome (Table 2). Genome scans assay for regions exhibiting unusual levels of divergence among populations or species that represent candidate selected alleles (Nielsen *et al.*, 2005; Yant *et al.*, 2013; Lotterhos and Whitlock, 2015; Jensen *et al.*, 2016). There are two main approaches to identify candidate loci: taking outliers of differentiation metrics or performing explicit hypothesis testing to determine whether the value is significantly greater than expected by chance or under neutrality. Genome scans can be confounded by other modes of selection and by effects of demography and are therefore best interpreted as hypothesis generators, providing candidate loci and processes to be tested in downstream functional studies, where possible. It may also be more confidently concluded that introgression is adaptive if a combination of methods, including descriptors of the genomic architecture of introgression and appropriately chosen selection metrics, converge on particular loci. In some cases, compelling *a priori* evidence that the trait is under similar directional selection in both species is also available. The combination of using methods assessing the genomic architecture of introgression and population genomics metrics was successfully applied when mining for adaptively introgressed candidate alleles for mediating adaptation to serpentine soils in *Arabidopsis* (Arnold *et al.*, 2016). In *Heliconius* butterflies there was *a priori* evidence for wing colour patterns involved in mimicry and mate recognition to be under directional selection in the hybridising species, and it was then shown that the introgressed alleles are responsible for this trait (Pardo-Díaz *et al.*, 2012).

Horizontal gene transfer events as a source of adaptive novelty

Alleles conferring an adaptive advantage may also be exchanged between reproductively isolated species via HGT. In prokaryotes HGT between distantly related species is well established as a source of novelty and a key driver of adaptation, most notably in the acquisition of antibiotic resistance and genes conferring pathogenicity (Gillings, 2017). Similarly, HGT has been shown to be prevalent among single-celled eukaryotes (Keeling and Palmer, 2008; Andersson, 2009). This penchant for HGT in prokaryotes has an ongoing effect on multicellular eukaryotes; HGT between the mitochondria of distantly related plant species is rampant (Won and Renner, 2003; Bergthorsson *et al.*, 2003; Mower *et al.*, 2010; Rice *et al.*, 2013). HGT in the plastid genome seems relatively infrequent, although there are cases (Rice *et al.*, 2006; Park *et al.*, 2007). This may be due to the fact that plant mitochondria have a mechanism for the active uptake of DNA and frequently fuse (Richardson and Palmer, 2007; Rice *et al.*, 2013), while plastids lack this tendency. HGT into the nuclear genomes of multicellular eukaryotes is less frequent. For any foreign DNA to be heritable it must be integrated into the germline, which is separated from the somatic cells and often protected from the environment by elaborate structures. Despite this, HGT does occur in the nuclear genomes

of multicellular eukaryotes; fungi (Ambrose *et al.*, 2014), arthropods (Wybouw *et al.*, 2016), nematodes (Danchin *et al.*, 2010), mosquitos (Klasson *et al.*, 2009), fish (Sun *et al.*, 2015), sea anemones (Starcevic *et al.*, 2008) and a broad range of plants (Bock, 2010) have all been shown to contain nuclear genes of HGT origin from diverse sources.

Many possible mechanisms for genetic transfers by HGT have been suggested. Lifestyle traits that allow intimate contact between unrelated species may increase the likelihood of HGT. For example, close contact between a host and its parasite, which can involve the exchange of macromolecules including mRNAs (Kim *et al.*, 2014), presents an opportunity for genetic exchange (Yoshida *et al.*, 2010; Xi *et al.*, 2012; Zhang *et al.*, 2013; Zhang *et al.*, 2014; Davis and Xi, 2015; Yang *et al.*, 2016) as does a reproductive cycle in which components of the germline are more exposed to the environment or even free living, such as those of bryophytes, lycophytes, and ferns (Li *et al.*, 2014). It has also been demonstrated that rare cases of grafting between unrelated species can result in the transformation of cells at the graft site (Bergthorsson, 2003; Stegemann, 2009; Stegemann *et al.* 2012). There are also many vectors that may transport genetic material between species, for example bacteria, viruses or mobile genetic elements. It has been established that pathogenic bacteria can transform eukaryotic host cells through the injection of proteins and/or genetic material (Lacroix and Citovsky, 2016). HGT of selfish genetic elements, such as transposons, is rampant and could mediate the movement of host DNA. Indeed, a study of group I introns in angiosperm mitochondria found 32 separate instances of HGT into plants (Cho *et al.*, 1998). Another study showed that 65% of the plant genomes analyzed contained at least one instance of HGT of a long terminal repeat retrotransposon (El Baidouri *et al.*, 2014). This likely has an important evolutionary function for selfish genetic elements, allowing them to escape resistant host genomes that effectively silence them. Finally, despite the complexity involved in shielding gametes from the environment in seed plants, it has been suggested that exposure to foreign pollen could result in small windows of opportunity for illegitimate pollination and HGT into the germline (Keeling and Palmer, 2008; Bock, 2010; Christin *et al.*, 2012).

A key outstanding question, however, is what, if any, is the adaptive impact of these HGT events? Arguably genes that do not confer an adaptive benefit are expected to decay by neutral drift, eventually to be relegated to pseudogene status and then lost altogether (Keeling and Palmer, 2008; Soucy, 2015). Many factors could render a gene acquired by HGT from a divergent organism useless, or even deleterious. A novel genetic background could abrogate interactions essential for gene function, while incompatible and divergent codon biases, transcriptional elements or intron/exon splice sites could also inactivate foreign genes. Indeed, the fate of many genes acquired by HGT in eukaryotes is decay (Bergthorsson, 2003; Mower *et al.*, 2010; Rice, 2013 Mahelka *et al.*, 2017). However, a large body of evidence suggests that this is not always the case (Emiliani *et al.*, 2009; Danchin *et al.*, 2010; Yue *et al.*, 2012; Christin *et al.*, 2012; Acuña *et al.*, 2012; Zhang *et al.*, 2013; Yang *et al.*, 2013; Li *et al.*, 2014; Ambrose

et al., 2014; Prentice *et al.*, 2015; Sun *et al.*, 2015; Yin *et al.*, 2016). The transcriptional and developmental regulation of horizontally transferred loci, alongside evidence for purifying or positive selection, suggests that many such events are adaptive.

Phylogenetic analysis is the gold standard for HGT inference (Keeling and Palmer, 2008; Brock, 2009; Soucy, 2015). It relies on detecting incongruence between individual locus trees and species phylogenies. Often these cases are obvious. However, alternative evolutionary processes as well as sampling and analytic errors can produce incongruent gene trees and these must be considered in each case. Several potential confounding causes include gene duplication and subsequent loss, inadequate taxonomic sampling, historical allopolyploidization and long branch attraction (Keeling and Palmer, 2008; Brock, 2009; Soucy 2015). Further the possibility exists of intracellular gene transfer from the mitochondrial and plastid genomes; thus, genes of alpha-proteobacterial or cyanobacterial origin should be excluded from analysis (Huang and Gogarten, 2008; Yang *et al.*, 2013). However, diverse evidence classes can corroborate candidate HGT events, such as codon usage differences, intron structure or GC content.

HGT and the emergence of land plants

Strong evidence implicates ancient HGT as a key source of adaptive novelty when the pioneering ancestor of green plants adapted to terrestrial environments (Huang and Gogarten, 2008; Emiliani *et al.*, 2009; Yue *et al.*, 2012; Yue *et al.*, 2013; Yang *et al.*, 2013). This lineage experienced an array of novel abiotic and biotic challenges upon colonisation of land, including desiccation, UV irradiation, and microbial attack. Analysis of the moss *Physcomitrella patens* identified 39 gene families that had been acquired by HGT from prokaryotes, fungi or viruses after the split between plants and green algae, 35 of which were shared with seed plants. These loci are involved in a broad range of plant-specific processes including biosynthesis, defence, stress tolerance, vascular development, and seed germination (Yue *et al.*, 2012; Yue *et al.*, 2013). In contrast to seed plants, the gametophytes and zygotes of mosses are more exposed to the environment, presenting an opportunity for the integration of foreign DNA. Another example is the phenylpropanoid pathway that produces compounds such as lignin and flavonoids, critical components in plant structure and defence against microbes and UV (Emiliani *et al.*, 2009). The common ancestor of land plants acquired the enzyme phenylpropanoid that performs the first critical step in this pathway via HGT from what was ultimately a bacterial source (Emiliani *et al.*, 2009). Another example is represented by the L-Ala-D/L-Glu epimerases (AEEs), which are ubiquitous in land plants and were initially acquired by HGT from prokaryotes (Yang *et al.*, 2013). The fixation of AEEs in land plants was driven by positive selection and was specific to land plants; they have not been found in any other eukaryotes including the extant progenitors of land plants, red and green algae (Yang *et al.*, 2013). Acquisition of genes by HGT prior to the split between red alga and green plants is also an important source of

Box 1: Established and promising model systems for adaptive introgression

It has long been the subject of debate whether introgression is more common in plants than other kingdoms (Mallet, 2005; Mallet, 2007). Introgression may be less common in animals compared with plants due to stronger assortative mating and lower F1 hybrid fitness. Interestingly, there are more animal than plant studies that find evidence for adaptive introgression (see Table 1): for example in animals, mussels (Fraïsse *et al.*, 2014), *Drosophila* (Garrigan *et al.*, 2012; Brand *et al.*, 2013; Llopart *et al.*, 2014; Beck *et al.*, 2015), *Anopheles* (Fontaine *et al.*, 2015; Norris *et al.*, 2015), *Heliconius* butterflies (Nadeau *et al.*, 2014; Zhang *et al.*, 2016), freshwater fish such as salmonids (Glover *et al.*, 2013; Ozerov *et al.*, 2016; Karlsson *et al.*, 2016), birds such as Darwin's finches (Lamichhaney *et al.*, 2015), mice (Song *et al.*, 2011; Staubach *et al.*, 2012), and humans (Racimo *et al.*, 2017); and in plants, *Arabidopsis* (Arnold *et al.*, 2016), sunflowers (Whitney *et al.*, 2015), *Senecio* (Kim *et al.*, 2008), and poplars (Suarez-Gonzalez *et al.*, 2016). This might be due to stronger economic/medical interest in animals, such as freshwater fish and malaria-transmitting mosquitos, resulting in more intense adaptive allele mining. However, this could also be due to higher rates of adaptive evolution in organisms with large effective population sizes (Gossmann *et al.*, 2010), such as *Drosophila*, *Anopheles*, *Heliconius* butterflies, some freshwater fish, as well as mice. Introgression may provide fertile ground for adaptive radiations (Seehausen, 2004), either by enriching genetic variation in an initial hybridization event between two species that may then fuel radiation or by introducing adaptations that allow species of radiating lineages to occupy new niches and further diversify. Introgression has been shown to partly drive the adaptive radiations of some plants, such as *Mimulus* (Stankowski and Streisfeld, 2015) and *Solanum* (Pease *et al.*, 2016), and some animals, such as Darwin's finches (Lamichhaney *et al.*, 2015) and cichlids (Meier *et al.*, 2017). Numerous cases of adaptive introgression are also reported for fungi, such as yeast (Dunn *et al.*, 2013; Almeida *et al.*, 2017), as well as *Albugo* (McMullan *et al.*, 2015).

genes involved in the functionality of plastids (Huang and Gogarten, 2008).

HGT mediating pathogen resistance and environmental adaptation

HGT is also a source of novelty that is exploited in pathogen resistance. For example, a gene important for virus resistance in domestic tomato is derived from the fusion of two genes, both of which were acquired by HGT ultimately from bacteria, although one of the genes appears to have passed through a fungus (Yang *et al.*, 2016). The obligatory parasite

Phelipanche aegyptiaca acquired an *albumin 1* gene, known to function as a storage protein and insect toxin, by HGT from legumes (Zhang *et al.*, 2013). Structural predictions, the conservation of key functional residues, and evidence of purifying selection all suggest that the gene serves an adaptive role. This HGT event was likely the result of historical host-parasite interactions. Another example is the fungus *Epichloë*, an intracellular plant symbiont, which repeatedly was conferred insect resistance to its hosts by an insect toxin acquired by the fungus via HGT from bacteria (Ambrose *et al.*, 2014).

The reverse is also true; HGT in plants, fungi, and insects has allowed enhanced pathogenic exploitation of plants. In the fungus responsible for apple canker, *Valsa mali*, multiple genes acquired by HGT from bacteria and fungi were implicated in pathogenicity with putative roles in the avoidance of host immune responses and the degradation of host tissues (Yin *et al.*, 2016). There is evidence that the berry borer beetle *Hypothenemus hampei* adapted to its role as a pathogen of coffee beans by the acquisition of the *HhMAN1* locus (Acuña *et al.*, 2012). The enzyme encoded is capable of breaking down galactomannan, the main storage polysaccharide in coffee beans and likely allows the beetles to exploit coffee beans as a food source. HGT has allowed plant-parasitic root knot nematodes to acquire a repertoire of plant cell wall degradation enzymes that facilitate parasitism from bacteria (Danchin *et al.*, 2010). Finally, a study of HGT in multiple parasitic plant lineages showed that genes acquired from the host via HGT are not only evolving under purifying or positive selection but are most likely to be expressed in the haustorium, the interface between host and parasite, implying they may have an adaptive role in host-parasite interactions (Yang *et al.*, 2016).

HGT has also been implicated in mediating repeated adaptation to stringent environmental conditions. C4 photosynthesis is a more efficient photosynthetic pathway in hot arid conditions that has evolved multiple times from C3 progenitors. In the *Alloteropsis* grasses, two key C4 photosynthesis proteins, phosphoenolpyruvate carboxylase and phosphoenolpyruvate carboxykinase, have been acquired by HGT at least four times from distantly related plants in close ecological contact with the grasses (Christin *et al.*, 2012). These pre-adapted C4 genes likely replaced their suboptimal homologues, rapidly optimizing the C4 pathway in the recipient. A metabolic enzyme with a key role in glucose metabolism that was acquired by plant-to-plant HGT has been shown to be associated with fine-scale biotic and abiotic environmental differences in the grass *Festuca ovina* (Prentice *et al.*, 2015).

A particularly striking example of adaptation mediated by HGT involves the photoreceptor neochrome, a chimeric photoreceptor originating from a gene fusion that is thought to play a pivotal role in the enhanced phototropic response of ferns, a key adaptive trait that allowed their diversification following the advent of angiosperms (Kawai *et al.*, 2003; Schneider *et al.*, 2004; Kanegae *et al.*, 2006; Schuettpelz and Pryer, 2009). This protein, previously thought to have arisen independently in ferns and algae, was initially acquired by the fern lineage through HGT from hornworts followed by subsequent inter-fern HGT (Li *et al.*, 2014). As discussed above, both ferns and hornworts have lifestyle traits that likely make

them more susceptible to HGT. Finally, there is evidence of HGT in commercially important species: domesticated sweet potato contains four transcribed *Agrobacterium* genes (Kyndt *et al.*, 2015) and the silkworm *Bombyx mori* contains 10 expressed genes from bacterial sources, with putative functions in disease resistance and metabolism (Zhu *et al.*, 2011).

Thus, HGT has had a profound impact on the genesis of many important adaptive plant traits such as the acquisition of endosymbionts, the origin of C4 photosynthesis, and the emergence of terrestrial plants. Compared with prokaryotes, HGT in eukaryotes is considered rare but the impact of such HGT events on the evolutionary trajectories of their recipients can be large. In this era of high-throughput sequencing technologies and especially whole genome sequencing, cases of HGT in multicellular eukaryotes are increasingly likely to be identified.

Near-term perspectives on adaptive allele mining using adaptive introgression

When phenotype-driven, allele mining for introgressed loci is a powerful tool for the identification of strong candidate alleles underlying particular adaptations. Indeed, we are at a watershed moment in the history of these approaches. There stands behind us a rich history, with long established model systems poised to be married to modern population genomics. It is now possible to detect loci under divergent selection, to test if the selected alleles have been introgressed and to associate these candidate alleles with phenotypes in ultra-high genomic resolution. In cases where these studies focus on clear phenotypes, it is obvious that such mixtures of approaches will engender rapid developments in understanding the mechanisms of adaptation (Box 1). Further, they stand to reveal the historic and geographic context of adaptive introgression mediating complex traits in the rich complexity presented by nature.

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References

- Abbott R, Albach D, Ansell S, *et al.* 2013. Hybridization and speciation. *Journal of Evolutionary Biology* **26**, 229–246.
- Acuña R, Padilla BE, Flórez-Ramos CP, *et al.* 2012. Adaptive horizontal transfer of a bacterial gene to an invasive insect pest of coffee. *Proceedings of the National Academy of Sciences, USA* **109**, 4197–4202.
- Ai H, Fang X, Yang B, *et al.* 2015. Adaptation and possible ancient interspecies introgression in pigs identified by whole-genome sequencing. *Nature Genetics* **47**, 217–225.
- Alexander DH, Novembre J, Lange K. 2009. Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* **19**, 1655–1664.
- Allendorf FW, Leary RF, Spruell P, Wenburg JK. 2001. The problems with hybrids: setting conservation guidelines. *Trends in Ecology and Evolution* **16**, 613–622.
- Almeida P, Barbosa R, Bensasson D, Gonçalves P, Sampaio JP. 2017. Adaptive divergence in wine yeasts and their wild relatives suggests a prominent role for introgressions and rapid evolution at noncoding sites. *Molecular Ecology* **26**, 2167–2182.
- Ambrose KV, Koppenhöfer AM, Belanger FC. 2014. Horizontal gene transfer of a bacterial insect toxin gene into the *Epichloë* fungal symbionts of grasses. *Scientific Reports* **4**, 5562.
- Anderson E. 1949. *Introgressive hybridization*. New York: John Wiley and Sons.
- Anderson E, Hubricht L. 1938. Hybridization in *Tradescantia*. III. The evidence for introgressive hybridization. *American Journal of Botany* **25**, 396–402.
- Anderson TM, vonHoldt BM, Candille SI, *et al.* 2009. Molecular and evolutionary history of melanism in North American gray wolves. *Science* **323**, 1339–1343.
- Andersson JO. 2009. Gene transfer and diversification of microbial eukaryotes. *Annual Review of Microbiology* **63**, 177–193.
- Arnold ML. 2016. *Divergence with genetic exchange*. Oxford: Oxford University Press.
- Arnold ML, Martin NH. 2009. Adaptation by introgression. *Journal of Biology* **8**, 82.
- Arnold BJ, Lahner B, DaCosta JM, Weisman CM, Hollister JD, Salt DE, Bomblies K, Yant L. 2016. Borrowed alleles and convergence in serpentine adaptation. *Proceedings of the National Academy of Sciences, USA* **113**, 8320–8325.
- Barton NH. 1979. The dynamics of hybrid zones. *Heredity* **43**, 341–359.
- Barton NH. 2001. The role of hybridization in evolution. *Molecular Ecology* **10**, 551–568.
- Barton NH, Hewitt GM. 1985. Analysis of hybrid zones. *Annual Review of Ecology, Evolution, and Systematics* **16**, 113–148.
- Barton NH, Hewitt GM. 1989. Adaptation, speciation and hybrid zones. *Nature* **341**, 497–503.
- Bastide H, Lange JD, Lack JB, Yassin A, Pool JE. 2016. A variable genetic architecture of melanistic evolution in *Drosophila melanogaster*. *Genetics* **204**, 1307–1319.
- Beck EA, Thompson AC, Sharbrough J, Brud E, Llopart A. 2015. Gene flow between *Drosophila yakuba* and *Drosophila santomea* in subunit V of cytochrome c oxidase: a potential case of cytonuclear cointrogression. *Evolution* **69**, 1973–1986.
- Berghthorsson U, Adams KL, Thomason B, Palmer JD. 2003. Widespread horizontal transfer of mitochondrial genes in flowering plants. *Nature* **424**, 197–201.
- Blischak PD, Kubatko LS, Wolfe AD. 2017. SNP genotyping and parameter estimation in polyploids using low-coverage sequencing data. *bioRxiv* doi: 10.1101/120261.
- Bock R. 2010. The give-and-take of DNA: horizontal gene transfer in plants. *Trends in Plant Science* **15**, 11–22.
- Bradburd GS, Ralph PL, Coop GM. 2016. A spatial framework for understanding population structure and admixture. *PLOS Genetics* **12**, e1005703.
- Brand CL, Kingan SB, Wu L, Garrigan D. 2013. A selective sweep across species boundaries in *Drosophila*. *Molecular Biology and Evolution* **30**, 2177–2186.
- Brennan AC, Bridle JR, Wang AL, Hiscock SJ, Abbott RJ. 2009. Adaptation and selection in the *Senecio* (Asteraceae) hybrid zone on Mount Etna, Sicily. *New Phytologist* **183**, 702–717.
- Brower AVZ. 2013. Introgression of wing pattern alleles and speciation via homoploid hybridization in *Heliconius* butterflies: a review of evidence from the genome. *Proceedings of the Royal Society B* **280**, 20122302.
- Buerkle CA, Lexer C. 2008. Admixture as the basis for genetic mapping. *Trends in Ecology & Evolution* **23**, 686–694.
- Burri R, Nater A, Kawakami T, *et al.* 2015. Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of *Ficedula* flycatchers. *Genome Research* **25**, 1656–1665.
- Chapman MA, Abbott RJ. 2010. Introgression of fitness genes across a ploidy barrier. *New Phytologist* **186**, 63–71.
- Cho Y, Qiu YL, Kuhlman P, Palmer JD. 1998. Explosive invasion of plant mitochondria by a group I intron. *Proceedings of the National Academy of Sciences, USA* **95**, 14244–14249.

- Christin PA, Edwards EJ, Besnard G, Boxall SF, Gregory R, Kellogg EA, Hartwell J, Osborne CP.** 2012. Adaptive evolution of C(4) photosynthesis through recurrent lateral gene transfer. *Current Biology* **22**, 445–449.
- Clark LV, Stewart JR, Nishiwaki A, et al.** 2015. Genetic structure of *Miscanthus sinensis* and *Miscanthus sacchariflorus* in Japan indicates a gradient of bidirectional but asymmetric introgression. *Journal of Experimental Botany* **66**, 4213–4225.
- Clarkson CS, Weetman D, Essandoh J, et al.** 2014. Adaptive introgression between *Anopheles* sibling species eliminates a major genomic island but not reproductive isolation. *Nature Communications* **5**, 4248.
- Coleman ML, Sullivan MB, Martiny AC, Steglich C, Barry K, Delong EF, Chisholm SW.** 2006. Genomic islands and the ecology and evolution of *Prochlorococcus*. *Science* **311**, 1768–1770.
- Coyne JA, Orr HA.** 2004. Speciation. Sunderland, Massachusetts: Sinauer Associates.
- Crawford JE, Nielsen R.** 2013. Detecting adaptive trait loci in nonmodel systems: divergence or admixture mapping? *Molecular Ecology* **22**, 6131–6148.
- Crispo E, Moore J-S, Lee-Yaw JA, Gray SM, Haller BC.** 2011. Broken barriers: human-induced changes to gene flow and introgression in animals. *BioEssays* **33**, 508–518.
- Cruickshank TE, Hahn MW.** 2014. Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow. *Molecular Ecology* **23**, 3133–3157.
- Cucchi T, Vigne J-D, Auffray J-C.** 2005. First occurrence of the house mouse (*Mus musculus domesticus* Schwarz & Schwarz, 1943) in the Western Mediterranean: a zooarchaeological revision of subfossil occurrences. *Biological Journal of the Linnean Society* **84**, 429–445.
- Danchin EGJ, Rosso M-N, Vieira P, de Almeida-Engler J, Coutinho PM, Henrissat B, Abad P.** 2010. Multiple lateral gene transfers and duplications have promoted plant parasitism ability in nematodes. *Proceedings of the National Academy of Sciences, USA* **107**, 17651–17656.
- Davis CC, Xi Z.** 2015. Horizontal gene transfer in parasitic plants. *Current Opinion in Plant Biology* **26**, 14–19.
- Délye C, Jasieniuk M, Le Corre V.** 2013. Deciphering the evolution of herbicide resistance in weeds. *Trends in Genetics* **29**, 649–658.
- den Nijs HCM, Bartsch D, Sweet J (eds.).** 2004. Introgression from genetically modified plants into wild relatives. Cambridge, Massachusetts: CABI Publishing.
- Dobzhansky T.** 1937. Genetics and the origin of species. New York: Columbia University Press.
- Dunn B, Paulish T, Stanbery A, et al.** 2013. Recurrent rearrangement during adaptive evolution in an interspecific yeast hybrid suggests a model for rapid introgression. *PLOS Genetics* **9**, e1003366.
- Durand EY, Patterson N, Reich D, Slatkin M.** 2011. Testing for ancient admixture between closely related populations. *Molecular Biology and Evolution* **28**, 2239–2252.
- Edmands S.** 2007. Between a rock and a hard place: evaluating the relative risks of inbreeding and outbreeding for conservation and management. *Molecular Ecology* **16**, 463–475.
- El Baidouri M, Carpentier MC, Cooke R, et al.** 2014. Widespread and frequent horizontal transfers of transposable elements in plants. *Genome Research* **24**, 831–838.
- Emiliani G, Fondi M, Fani R, Gribaldo S.** 2009. A horizontal gene transfer at the origin of phenylpropanoid metabolism: a key adaptation of plants to land. *Biology Direct* **4**, 7.
- Endler JA.** 1977. Geographic variation, speciation and clines. Monographs in Population Biology, No. **10**, Princeton, New Jersey: Princeton University Press.
- Excoffier L, Dupanloup I, Huerta-Sánchez E, Sousa VC, Foll M.** 2013. Robust demographic inference from genomic and SNP data. *PLOS Genetics* **9**, e1003905.
- Feder JL, Egan SP, Nosil P.** 2012. The genomics of speciation-with-gene-flow. *Trends in Genetics* **28**, 342–350.
- Feder JL, Nosil P.** 2009. Chromosomal inversions and species differences: when are genes affecting adaptive divergence and reproductive isolation expected to reside within inversions? *Evolution* **63**, 3061–3075.
- Filatov DA, Osborne OG, Papadopoulos AS.** 2016. Demographic history of speciation in a *Senecio* altitudinal hybrid zone on Mt. Etna. *Molecular Ecology* **25**, 2467–2481.
- Fitzpatrick BM, Johnson JR, Kump DK, Smith JJ, Voss SR, Shaffer HB.** 2010. Rapid spread of invasive genes into a threatened native species. *Proceedings of the National Academy of Sciences, USA* **107**, 3606–3610.
- Fontaine MC, Pease JB, Steele A, et al.** 2015. Extensive introgression in a malaria vector species complex revealed by phylogenomics. *Science* **347**, 1258524.
- Fontdevila A.** 2005. Hybrid genome evolution by transposition. *Cytogenetic and Genome Research* **110**, 49–55.
- Fraïsse C, Belkhir K, Welch JJ, Bierne N.** 2016. Local interspecies introgression is the main cause of extreme levels of intraspecific differentiation in mussels. *Molecular Ecology* **25**, 269–286.
- Fraïsse C, Roux C, Welch JJ, Bierne N.** 2014. Gene-flow in a mosaic hybrid zone: is local introgression adaptive? *Genetics* **197**, 939–951.
- Garrigan D, Kingan SB, Geneva AJ, Andolfatto P, Clark AG, Thornton KR, Presgraves DC.** 2012. Genome sequencing reveals complex speciation in the *Drosophila simulans* clade. *Genome Research* **22**, 1499–1511.
- Gillings MR.** 2017. Lateral gene transfer, bacterial genome evolution, and the Anthropocene. *Annals of the New York Academy of Sciences* **1389**, 20–36.
- Glover KA, Pertoldi C, Besnier F, Wennevik V, Kent M, Skaala Ø.** 2013. Atlantic salmon populations invaded by farmed escapees: quantifying genetic introgression with a Bayesian approach and SNPs. *BMC Genetics* **14**, 74.
- Gómez JM, González-Megías A, Lorite J, Abdelaziz M, Perfectti F.** 2015. The silent extinction: climate change and the potential hybridization-mediated extinction of endemic high-mountain plants. *Biodiversity and Conservation* **24**, 1843–1857.
- Gompert Z, Buerkle CA.** 2016. What, if anything, are hybrids: enduring truths and challenges associated with population structure and gene flow. *Evolutionary Applications* **9**, 909–923.
- Gossmann TI, Song BH, Windsor AJ, Mitchell-Olds T, Dixon CJ, Kapralov MV, Filatov DA, Eyre-Walker A.** 2010. Genome wide analyses reveal little evidence for adaptive evolution in many plant species. *Molecular Biology and Evolution* **27**, 1822–1832.
- Green RE, Krause J, Briggs AW, et al.** 2010. A draft sequence of the Neandertal genome. *Science* **328**, 710–722.
- Guénet JL, Bonhomme F.** 2003. Wild mice: an ever-increasing contribution to a popular mammalian model. *Trends in Genetics* **19**, 24–31.
- Gutenkunst RN, Hernandez RD, Williamson SH, Bustamante CD.** 2009. Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data. *PLOS Genetics* **5**, e1000695.
- Hamilton JA, De la Torre AR, Aitken SN.** 2015. Fine-scale environmental variation contributes to introgression in a three-species spruce hybrid complex. *Tree Genetics and Genomes* **11**, 817.
- Hamilton JA, Lexer C, Aitken SN.** 2013. Differential introgression reveals candidate genes for selection across a spruce (*Picea sitchensis* × *P. glauca*) hybrid zone. *New Phytologist* **197**, 927–938.
- Han TS, Wu Q, Hou XH, Li ZW, Zou YP, Ge S, Guo YL.** 2015. Frequent introgressions from diploid species contribute to the adaptation of the tetraploid Shepherd's purse (*Capsella bursa-pastoris*). *Molecular Plant* **8**, 427–438.
- Hand BK, Lowe WH, Kovach RP, Muhlfeld CC, Luikart G.** 2015. Landscape community genomics: understanding eco-evolutionary processes in complex environments. *Trends in Ecology & Evolution* **30**, 161–168.
- Harr B.** 2006. Genomic islands of differentiation between house mouse subspecies. *Genome Research* **16**, 730–737.
- Harrison RG.** 1986. Pattern and process in a narrow hybrid zone. *Heredity* **56**, 337–349.
- Harrison RG.** 1990. Hybrid zones: windows on evolutionary process. In: Futuyma D, Antonovics J, eds., *Oxford surveys in evolutionary biology*, Oxford: Oxford University Press, 69–128.

- Harrison RG.** 2012. The language of speciation. *Evolution* **66**, 3643–3657.
- Harrison RG, Larson EL.** 2014. Hybridization, introgression, and the nature of species boundaries. *Journal of Heredity* **105**, 795–809.
- Hedrick PW.** 2013. Adaptive introgression in animals: examples and comparison to new mutation and standing variation as sources of adaptive variation. *Molecular Ecology* **22**, 4606–4618.
- Hewitt GM.** 1975. A sex-chromosome hybrid zone in the grasshopper *Podisma pedestris* (Orthoptera: Acrididae). *Heredity* **35**, 375–387.
- Hewitt GM.** 1988. Hybrid zones-natural laboratories for evolutionary studies. *Trends in ecology & evolution* **3**, 158–167.
- Hey J.** 2010a. Isolation with migration models for more than two populations. *Molecular Biology and Evolution* **27**, 905–920.
- Hey J.** 2010b. The divergence of chimpanzee species and subspecies as revealed in multipopulation isolation-with-migration analyses. *Molecular Biology and Evolution* **27**, 921–933.
- Hey J, Nielsen R.** 2007. Integration within the Felsenstein equation for improved Markov chain Monte Carlo methods in population genetics. *Proceedings of the National Academy of Sciences, USA* **104**, 2785–2790.
- Hohenlohe PA, Bassham S, Currey M, Cresko WA.** 2012. Extensive linkage disequilibrium and parallel adaptive divergence across threespine stickleback genomes. *Philosophical Transactions of the Royal Society B* **367**, 395–408.
- Hohenlohe PA, Day MD, Amish SJ, et al.** 2013. Genomic patterns of introgression in rainbow and westslope cutthroat trout illuminated by overlapping paired-end RAD sequencing. *Molecular Ecology* **22**, 3002–3013.
- Hohmann N, Wolf EM, Lysak MA, Koch MA.** 2015. A time-calibrated road map of brassicaceae species radiation and evolutionary history. *The Plant Cell* **27**, 2770–2784.
- Huang J, Gogarten JP.** 2008. Concerted gene recruitment in early plant evolution. *Genome Biology* **9**, R109.
- Hubisz MJ, Falush D, Stephens M, Pritchard JK.** 2009. Inferring weak population structure with the assistance of sample group information. *Molecular Ecology Resources* **9**, 1322–1332.
- Huerta-Sánchez E, Jin X, Asan, et al.** 2014. Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. *Nature* **512**, 194–197.
- Hufford MB, Lubinsky P, Pyhäjärvi T, Devengenzo MT, Ellstrand NC, Ross-Ibarra J.** 2013. The genomic signature of crop-wild introgression in maize. *PLOS Genetics* **9**, e1003477.
- Hufford MB, Xu X, van Heerwaarden J, et al.** 2012. Comparative population genomics of maize domestication and improvement. *Nature Genetics* **44**, 808–811.
- Huson DH, Bryant D.** 2006. Application of phylogenetic networks in evolutionary studies. *Molecular Biology and Evolution* **23**, 254–267.
- Jensen JD, Foll M, Bernatchez L.** 2016. Special issue: detecting selection in natural populations. *Molecular Ecology* **25**, 1–430.
- Jeong C, Alkorta-Aranburu G, Basnyat B, Neupane M, Witonsky DB, Pritchard JK, Beall CM, Di Rienzo A.** 2014. Admixture facilitates genetic adaptations to high altitude in Tibet. *Nature Communications* **5**, 3281.
- Jombart T.** 2008. adegenet: a R package for the multivariate analysis of genetic markers. *Bioinformatics* **24**, 1403–1405.
- Jombart T, Devillard S, Balloux F.** 2010. Discriminant analysis of principal components: a new method for the analysis of genetically structured populations. *BMC Genetics* **11**, 94.
- Jónsson H, Schubert M, Seguin-Orlando A, et al.** 2014. Speciation with gene flow in equids despite extensive chromosomal plasticity. *Proceedings of the National Academy of Sciences, USA* **111**, 18655–18660.
- Kanegae T, Hayashida E, Kuramoto C, Wada M.** 2006. A single chromoprotein with triple chromophores acts as both a phytochrome and a phototropin. *Proceedings of the National Academy of Sciences, USA* **103**, 17997–18001.
- Karasov T, Messer PW, Petrov DA.** 2010. Evidence that adaptation in *Drosophila* is not limited by mutation at single sites. *PLOS Genetics* **6**, e1000924.
- Karlsson S, Diserud OH, Fiske P, Hindar K.** 2016. Widespread genetic introgression of escaped farmed Atlantic salmon in wild salmon populations. *ICES Journal of Marine Science* **73**, 2488–2498.
- Kawai H, Kanegae T, Christensen S, Kiyosue T, Sato Y, Imaizumi T, Kadota A, Wada M.** 2003. Responses of ferns to red light are mediated by an unconventional photoreceptor. *Nature* **421**, 287–290.
- Keeling PJ, Palmer JD.** 2008. Horizontal gene transfer in eukaryotic evolution. *Nature reviews. Genetics* **9**, 605–618.
- Kellis M, Patterson N, Endrizzi M, Birren B, Lander ES.** 2003. Sequencing and comparison of yeast species to identify genes and regulatory elements. *Nature* **423**, 241–254.
- Kim M, Cui M-L, Cubas P, Gillies A, Lee K, Chapman MA, Abbott RJ, Coen E.** 2008. Regulatory genes control a key morphological and ecological trait transferred between species. *Science* **322**, 1116–1119.
- Kim G, LeBlanc ML, Wafula EK, dePamphilis CW, Westwood JH.** 2014. Genomic-scale exchange of mRNA between a parasitic plant and its hosts. *Science* **345**, 808–811.
- Klasson L, Kambris Z, Cook PE, Walker T, Sinkins SP.** 2009. Horizontal gene transfer between *Wolbachia* and the mosquito *Aedes aegypti*. *BMC Genomics* **10**, 33.
- Kovach RP, Hand BK, Hohenlohe PA, et al.** 2016. Vive la résistance: genome-wide selection against introduced alleles in invasive hybrid zones. *Proceedings of the Royal Society B* **283**, 20161380.
- Kovach RP, Muhlfeld CC, Boyer MC, Lowe WH, Allendorf FW, Luikart G.** 2015. Dispersal and selection mediate hybridization between a native and invasive species. *Proceedings of the Royal Society B* **282**, 20142454.
- Kozak KM, Wahlberg N, Neild AF, Dasmahapatra KK, Mallet J, Jiggins CD.** 2015. Multilocus species trees show the recent adaptive radiation of the mimetic heliconius butterflies. *Systematic Biology* **64**, 505–524.
- Kronforst MR, Hansen ME, Crawford NG, Gallant JR, Zhang W, Kulathinal RJ, Kapan DD, Mullen SP.** 2013. Hybridization reveals the evolving genomic architecture of speciation. *Cell Reports* **5**, 666–677.
- Kumar V, Lammers F, Bidon T, Pfenninger M, Kolter L, Nilsson MA, Janke A.** 2017. The evolutionary history of bears is characterized by gene flow across species. *Scientific Reports* **7**, 46487.
- Kyndt T, Quispe D, Zhai H, Jarret R, Ghislain M, Liu Q, Gheysen G, Kreuze JF.** 2015. The genome of cultivated sweet potato contains *Agrobacterium* T-DNAs with expressed genes: An example of a naturally transgenic food crop. *Proceedings of the National Academy of Sciences, USA* **112**, 5844–5849.
- Lacroix B, Citovsky V.** 2016. Transfer of DNA from bacteria to eukaryotes. *mBio* **7**, 1–9.
- Lafon-Placette C, Johannessen IM, Hornslien KS, et al.** 2017. Endosperm-based hybridization barriers explain the pattern of gene flow between *Arabidopsis lyrata* and *Arabidopsis arenosa* in Central Europe. *Proceedings of the National Academy of Sciences, USA* **114**, E1027–E1035.
- Lamichhaney S, Berglund J, Almén MS, et al.** 2015. Evolution of Darwin's finches and their beaks revealed by genome sequencing. *Nature* **518**, 371–375.
- Laval G, Excoffier L.** 2004. SIMCOAL 2.0: a program to simulate genomic diversity over large recombining regions in a subdivided population with a complex history. *Bioinformatics* **20**, 2485–2487.
- Lawson DJ, Hellenthal G, Myers S, Falush D.** 2012. Inference of population structure using dense haplotype data. *PLOS Genetics* **8**, e1002453.
- Lee Y, Collier TC, Sanford MR, Marsden CD, Fofana A, Cornel AJ, Lanzaro GC.** 2013. Chromosome inversions, genomic differentiation and speciation in the African malaria mosquito *Anopheles gambiae*. *PLOS One* **8**, e57887.
- Lee Y, Marsden CD, Norris LC, Collier TC, Main BJ, Fofana A, Cornel AJ, Lanzaro GC.** 2013b. Spatiotemporal dynamics of gene flow and hybrid fitness between the M and S forms of the malaria mosquito, *Anopheles gambiae*. *Proceedings of the National Academy of Sciences, USA* **110**, 19854–19859.
- Lee CR, Svoldal H, Farlow A, Exposito-Alonso M, Ding W, Novikova P, Alonso-Blanco C, Weigel D, Nordborg M.** 2017. On the post-glacial spread of human commensal *Arabidopsis thaliana*. *Nature Communications* **8**, 14458.
- Levens ND, Tiffin P, Olson MS.** 2012. Pleistocene speciation in the genus *Populus* (salicaceae). *Systematic Biology* **61**, 401–412.

- Li YF, Costello JC, Holloway AK, Hahn MW. 2008. "Reverse ecology" and the power of population genomics. *Evolution* **62**, 2984–2994.
- Li H, Durbin R. 2011. Inference of human population history from whole genome sequence of a single individual. *Nature* **475**, 493–496.
- Li F-W, Villarreal JC, Kelly S, *et al.* 2014. Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. *Proceedings of the National Academy of Sciences, USA* **111**, 6672–6677.
- Liu S, Li F, Kong L, Sun Y, Qin L, Chen S, Cui H, Huang Y, Xia G. 2015. Genetic and epigenetic changes in somatic hybrid introgression lines between wheat and tall wheatgrass. *Genetics* **199**, 1035–1045.
- Liu Z, Wang Y, Shen Y, Guo W, Hao S, Liu B. 2004. Extensive alterations in DNA methylation and transcription in rice caused by introgression from *Zizania latifolia*. *Plant Molecular Biology* **54**, 571–582.
- Llopart A, Elwyn S, Lachaise D, Coyne JA. 2002. Genetics of a difference in pigmentation between *Drosophila yakuba* and *Drosophila santomea*. *Evolution* **56**, 2262–2277.
- Llopart A, Herrig D, Brud E, Stecklein Z. 2014. Sequential adaptive introgression of the mitochondrial genome in *Drosophila yakuba* and *Drosophila santomea*. *Molecular Ecology* **23**, 1124–1136.
- Long A, Liti G, Luptak A, Tenaillon O. 2015. Elucidating the molecular architecture of adaptation via evolve and resequence experiments. *Nature reviews. Genetics* **16**, 567–582.
- Lotterhos KE, Whitlock MC. 2015. The relative power of genome scans to detect local adaptation depends on sampling design and statistical method. *Molecular Ecology* **24**, 1031–1046.
- Mahelka V, Krak K, Kopecký D, Fehrer J, Šafář J, Bartoš J, Hobza R, Blavet N, Blattner FR. 2017. Multiple horizontal transfers of nuclear ribosomal genes between phylogenetically distinct grass lineages. *Proceedings of the National Academy of Sciences, USA* **114**, 1726–1731.
- Malinsky M, Challis RJ, Tyers AM, *et al.* 2015. Genomic islands of speciation separate cichlid ecomorphs in an East African crater lake. *Science* **350**, 1493–1498.
- Mallet J. 2005. Hybridization as an invasion of the genome. *Trends in ecology & evolution* **20**, 229–237.
- Mallet J. 2007. Hybrid speciation. *Nature* **446**, 279–283.
- Mallet J, Barton N, Lamas G, Santisteban J, Muedas M, Eeley H. 1990. Estimates of selection and gene flow from measures of cline width and linkage disequilibrium in *Heliconius* hybrid zones. *Genetics* **124**, 921–936.
- Mallet J, Besansky N, Hahn MW. 2016. How reticulated are species? *BioEssays* **38**, 140–149.
- Marques DA, Lucek K, Meier JI, Mwaiko S, Wagner CE, Excoffier L, Seehausen O. 2016. Genomics of Rapid Incipient Speciation in Sympatric Threespine Stickleback. *PLOS Genetics* **12**, e1005887.
- Martin SH, Dasmahapatra KK, Nadeau NJ, *et al.* 2013. Genome-wide evidence for speciation with gene flow in *Heliconius* butterflies. *Genome Research* **23**, 1817–1828.
- Martin SH, Davey JW, Jiggins CD. 2015. Evaluating the use of ABBA-BABA statistics to locate introgressed loci. *Molecular Biology and Evolution* **32**, 244–257.
- Martin SH, Van Belleghem SM. 2017. Exploring evolutionary relationships across the genome using topology weighting. *Genetics* **206**, 429–438.
- Mayr E. 1942. *Systematics and the origin of species*. New York: Columbia University Press.
- McMullan M, Gardiner A, Bailey K, *et al.* 2015. Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of *Albugo candida*, a generalist parasite. *eLife* **4**: e04550.
- Meier JI, Marques DA, Mwaiko S, Wagner CE, Excoffier L, Seehausen O. 2017. Ancient hybridization fuels rapid cichlid fish adaptive radiations. *Nature Communications* **8**, 14363.
- Meyer M, Kircher M, Gansauge M-T, *et al.* 2012. A high coverage genome sequence from an archaic Denisovan individual. *Science* **338**, 222–226.
- Michel AP, Sim S, Powell TH, Taylor MS, Nosil P, Feder JL. 2010. Widespread genomic divergence during sympatric speciation. *Proceedings of the National Academy of Sciences, USA* **107**, 9724–9729.
- Moore WS. 1977. An evaluation of narrow hybrid zones in vertebrates. *The Quarterly Review of Biology* **52**, 263–277.
- Morales AE, Jackson ND, Dewey TA, O'Meara BC, Carstens BC. 2017. Speciation with gene flow in north american *Myotis* bats. *Systematic Biology* **66**, 440–452.
- Mower JP, Stefanović S, Hao W, Gummow JS, Jain K, Ahmed D, Palmer JD. 2010. Horizontal acquisition of multiple mitochondrial genes from a parasitic plant followed by gene conversion with host mitochondrial genes. *BMC Biology* **8**, 150.
- Muhlfeld CC, Kovach RP, Jones LA, Al-Chokhachy R, Boyer MC, Leary RF, Lowe WH, Luikart G, Allendorf FW. 2014. Invasive hybridization in a threatened species is accelerated by climate change. *Nature Climate Change* **4**, 620–624.
- Nadeau NJ, Martin SH, Kozak KM, *et al.* 2013. Genome-wide patterns of divergence and gene flow across a butterfly radiation. *Molecular Ecology* **22**, 814–826.
- Nadeau NJ, Ruiz M, Salazar P, *et al.* 2014. Population genomics of parallel hybrid zones in the mimetic butterflies, *H. melpomene* and *H. erato*. *Genome Research* **24**, 1316–1333.
- Nielsen R, Williamson S, Kim Y, Hubisz MJ, Clark AG, Bustamante C. 2005. Genomic scans for selective sweeps using SNP data. *Genome Research* **15**, 1566–1575.
- Noor MA, Bennett SM. 2009. Islands of speciation or mirages in the desert? Examining the role of restricted recombination in maintaining species. *Heredity* **103**, 439–444.
- Noor MAF, Grams KL, Bertucci LA, Reiland J. 2001. Chromosomal inversions and the reproductive isolation of species. *Proceedings of the National Academy of Sciences, USA* **98**, 12084–12088.
- Norris LC, Main BJ, Lee Y, Collier TC, Fofana A, Cornel AJ, Lanzaro GC. 2015. Adaptive introgression in an African malaria mosquito coincident with the increased usage of insecticide-treated bed nets. *Proceedings of the National Academy of Sciences, USA* **112**, 815–820.
- Nosil P. 2008. Speciation with gene flow could be common. *Molecular Ecology* **17**, 2103–2106.
- Nosil P, Schluter D. 2011. The genes underlying the process of speciation. *Trends in Ecology & Evolution* **26**, 160–167.
- Olson-Manning CF, Wagner MR, Mitchell-Olds T. 2012. Adaptive evolution: evaluating empirical support for theoretical predictions. *Nature reviews. Genetics* **13**, 867–877.
- Orr HA, Masly JP, Presgraves DC. 2004. Speciation genes. *Current Opinion in Genetics & Development* **14**, 675–679.
- Ottoni C, Van Neer W, De Cupere B, *et al.* 2017. The palaeogenetics of cat dispersal in the ancient world. *Nature Ecology and Evolution* **1**, 0139.
- Ozerov MY, Gross R, Bruneaux M, Vähä JP, Burimski O, Pukk L, Vasemägi A. 2016. Genomewide introgressive hybridization patterns in wild Atlantic salmon influenced by inadvertent gene flow from hatchery releases. *Molecular Ecology* **25**, 1275–1293.
- Paaby AB, Rockman MV. 2014. Cryptic genetic variation: evolution's hidden substrate. *Nature reviews. Genetics* **15**, 247–258.
- Pallares LF, Harr B, Turner LM, Tautz D. 2014. Use of a natural hybrid zone for genomewide association mapping of craniofacial traits in the house mouse. *Molecular Ecology* **23**, 5756–5770.
- Pallares LF, Turner LM, Tautz D. 2016. Craniofacial shape transition across the house mouse hybrid zone: implications for the genetic architecture and evolution of between-species differences. *Development Genes and Evolution* **226**, 173–186.
- Pardo-Diaz C, Salazar C, Baxter SW, Merot C, Figueiredo-Ready W, Joron M, McMillan WO, Jiggins CD. 2012. Adaptive introgression across species boundaries in *Heliconius* butterflies. *PLOS Genetics* **8**, e1002752.
- Parisod C, Defnod C, Sarr A, Arrigo N, Felber F. 2013. Genome-specific introgression between wheat and its wild relative *Aegilops triuncialis*. *Journal of Evolutionary Biology* **26**, 223–228.
- Park JM, Manen JF, Schneeweiss GM. 2007. Horizontal gene transfer of a plastid gene in the non-photosynthetic flowering plants *Orobanchae* and *Phelipanche* (Orobanchaceae). *Molecular Phylogenetics and Evolution* **43**, 974–985.
- Pease JB, Haak DC, Hahn MW, Moyle LC. 2016. Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation. *PLOS Biology* **14**, e1002379.

- Pease JB, Hahn MW.** 2015. Detection and polarization of introgression in a five-taxon phylogeny. *Systematic Biology* **64**, 651–662.
- Pickrell JK, Pritchard JK.** 2012. Inference of population splits and mixtures from genome-wide allele frequency data. *PLOS Genetics* **8**, e1002967.
- Pinheiro F, De Barros F, Palma-Silva C, Meyer D, Fay MF, Suzuki RM, Lexer C, Cozzolino S.** 2010. Hybridization and introgression across different ploidy levels in the Neotropical orchids *Epidendrum fulgens* and *E. puniceoluteum* (Orchidaceae). *Molecular Ecology* **19**, 3981–3994.
- Vaz Pinto P, Beja P, Ferrand N, Godinho R.** 2016. Hybridization following population collapse in a critically endangered antelope. *Scientific Reports* **6**, 18788.
- Prentice HC, Li Y, Lönn M, Tunlid A, Ghatnekar L.** 2015. A horizontally transferred nuclear gene is associated with microhabitat variation in a natural plant population. *Proceedings of the Royal Society B* **282**, 20152453.
- Pritchard JK, Stephens M, Donnelly P.** 2000. Inference of population structure using multilocus genotype data. *Genetics* **155**, 945–959.
- Racimo F, Marnetto D, Huerta-Sánchez E.** 2017. Signatures of archaic adaptive introgression in present-day human populations. *Molecular Biology and Evolution* **34**, 296–317.
- Raj A, Stephens M, Pritchard JK.** 2014. fastSTRUCTURE: variational inference of population structure in large SNP data sets. *Genetics* **197**, 573–589.
- Ramsey J, Schemske DW.** 1998. Pathways, mechanisms, and rates of polyploid formation in flowering plants. *Annual Review of Ecology, Evolution, and Systematics* **29**, 467–501.
- Renaut S, Grassa CJ, Yeaman S, Moyers BT, Lai Z, Kane NC, Bowers JE, Burke JM, Rieseberg LH.** 2013. Genomic islands of divergence are not affected by geography of speciation in sunflowers. *Nature Communications* **4**, 1827.
- Rice DW, Alverson AJ, Richardson AO, et al.** 2013. Horizontal transfer of entire genomes via mitochondrial fusion in the angiosperm *Amborella*. *Science* **342**, 1468–1473.
- Rice DW, Palmer JD.** 2006. An exceptional horizontal gene transfer in plastids: gene replacement by a distant bacterial paralog and evidence that haptophyte and cryptophyte plastids are sisters. *BMC Biology* **4**, 31.
- Richardson AO, Palmer JD.** 2007. Horizontal gene transfer in plants. *Journal of Experimental Botany* **58**, 1–9.
- Rieseberg LH.** 2001. Chromosomal rearrangements and speciation. *Trends in Ecology & Evolution* **16**, 351–358.
- Rieseberg LH, Blackman BK.** 2010. Speciation genes in plants. *Annals of Botany* **106**, 439–455.
- Rieseberg LH, Buerkle CA.** 2002. Genetic mapping in hybrid zones. *The American Naturalist* **159**(Suppl 3), S36–S50.
- Rougeux C, Bernatchez L, Gagnaire P-A.** 2016. Modeling the multiple facets of speciation-with-gene-flow towards inferring the divergence history of lake whitefish species pairs (*Coregonus clupeaformis*). *bioRxiv* doi: 10.1101/068932.
- Roux C, Fraïsse C, Castric V, Vekemans X, Pogson GH, Bierne N.** 2014. Can we continue to neglect genomic variation in introgression rates when inferring the history of speciation? A case study in a *Mytilus* hybrid zone. *Journal of Evolutionary Biology* **27**, 1662–1675.
- Royer AM, Streisfeld MA, Smith CI.** 2016. Population genomics of divergence within an obligate pollination mutualism: Selection maintains differences between Joshua tree species. *American Journal of Botany* **103**, 1730–1741.
- Saarman NP, Pogson GH.** 2015. Introgression between invasive and native blue mussels (genus *Mytilus*) in the central California hybrid zone. *Molecular Ecology* **24**, 4723–4738.
- Sankararaman S, Mallick S, Dannemann M, Prüfer K, Kelso J, Pääbo S, Patterson N, Reich D.** 2014. The landscape of Neandertal ancestry in present-day humans. *Nature* **507**, 354–357.
- Sankararaman S, Patterson N, Li H, Pääbo S, Reich D.** 2012. The date of interbreeding between Neandertals and modern humans. *PLOS Genetics* **8**, e1002947.
- Scascitelli M, Whitney KD, Randell RA, King M, Buerkle CA, Rieseberg LH.** 2010. Genome scan of hybridizing sunflowers from Texas (*Helianthus annuus* and *H. debilis*) reveals asymmetric patterns of introgression and small islands of genomic differentiation. *Molecular Ecology* **19**, 521–541.
- Schiffels S, Durbin R.** 2014. Inferring human population size and separation history from multiple genome sequences. *Nature Genetics* **46**, 919–925.
- Schiffels S, Haak W, Paajanen P, Llamas B, Popescu E, Loe L, Clarke R, Lyons A, Mortimer R, Sayer D, Tyler-Smith C, Cooper A, Durbin R.** 2016. Iron Age and Anglo-Saxon genomes from East England reveal British migration history. *Nature Communications* **7**, 10408.
- Schneider H, Schuettpelz E, Pryer KM, Cranfill R, Magallón S, Lupia R.** 2004. Ferns diversified in the shadow of angiosperms. *Nature* **428**, 553–557.
- Schuettpelz E, Pryer KM.** 2009. Evidence for a Cenozoic radiation of ferns in an angiosperm-dominated canopy. *Proceedings of the National Academy of Sciences of the United States of America* **106**, 11200–11205.
- Schmickl R, Koch MA.** 2011. *Arabidopsis* hybrid speciation processes. *Proceedings of the National Academy of Sciences of the United States of America* **108**, 14192–14197.
- Seehausen O.** 2004. Hybridization and adaptive radiation. *Trends in ecology & evolution* **19**, 198–207.
- Shapiro BJ, Leducq JB, Mallet J.** 2016. What Is Speciation? *PLOS Genetics* **12**, e1005860.
- Smith J, Kronforst MR.** 2013. Do *Heliconius* butterfly species exchange mimicry alleles? *Biology Letters* **9**, 20130503.
- Song Y, Endepols S, Klemann N, Richter D, Matuschka FR, Shih CH, Nachman MW, Kohn MH.** 2011. Adaptive introgression of anticoagulant rodent poison resistance by hybridization between old world mice. *Current Biology: CB* **21**, 1296–1301.
- Soucy SM, Huang J, Gogarten JP.** 2015. Horizontal gene transfer: building the web of life. *Nature Reviews. Genetics* **16**, 472–482.
- Stankowski S, Streisfeld MA.** 2015. Introgressive hybridization facilitates adaptive divergence in a recent radiation of monkeyflowers. *Proceedings of the Royal Society B* **282**, 20151666.
- Starcevic A, Akthar S, Dunlap WC, Shick JM, Hranueli D, Cullum J, Long PF.** 2008. Enzymes of the shikimic acid pathway encoded in the genome of a basal metazoan, *Nematostella vectensis*, have microbial origins. *Proceedings of the National Academy of Sciences, USA* **105**, 2533–2537.
- Staubach F, Lorenc A, Messer PW, Tang K, Petrov DA, Tautz D.** 2012. Genome patterns of selection and introgression of haplotypes in natural populations of the house mouse (*Mus musculus*). *PLOS Genetics* **8**, e1002891.
- Stegemann S, Bock R.** 2009. Exchange of genetic material between cells in plant tissue grafts. *Science* **324**, 649–651.
- Stegemann S, Keuthe M, Greiner S, Bock R.** 2012. Horizontal transfer of chloroplast genomes between plant species. *Proceedings of the National Academy of Sciences of the United States of America* **109**, 2434–2438.
- Stebbins GL.** 1971. Chromosomal evolution in higher plants. London: Edward Arnold Ltd.
- Suarez-Gonzalez A, Hefer CA, Christe C, Corea O, Lexer C, Cronk QC, Douglas CJ.** 2016. Genomic and functional approaches reveal a case of adaptive introgression from *Populus balsamifera* (balsam poplar) in *P. trichocarpa* (black cottonwood). *Molecular Ecology* **25**, 2427–2442.
- Sun BF, Li T, Xiao JH, Jia LY, Liu L, Zhang P, Murphy RW, He SM, Huang DW.** 2015. Horizontal functional gene transfer from bacteria to fishes. *Scientific Reports* **5**, 18676.
- Supple MA, Papa R, Hines HM, McMillan WO, Counterman BA.** 2015. Divergence with gene flow across a speciation continuum of *Heliconius* butterflies. *BMC Evolutionary Biology* **15**, 204.
- Taylor SA, Larson EL, Harrison RG.** 2015. Hybrid zones: windows on climate change. *Trends in Ecology & Evolution* **30**, 398–406.
- Than C, Ruths D, Nakhleh L.** 2008. PhyloNet: a software package for analyzing and reconstructing reticulate evolutionary relationships. *BMC Bioinformatics* **9**, 322.
- The *Heliconius* Genome Consortium.** 2012. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature* **487**, 94–98.

- Todesco M, Pascual MA, Owens GL, et al.** 2016. Hybridization and extinction. *Evolutionary Applications* **9**, 892–908.
- Turner TL, Hahn MW.** 2010. Genomic islands of speciation or genomic islands and speciation? *Molecular Ecology* **19**, 848–850.
- Turner TL, Hahn MW, Nuzhdin SV.** 2005. Genomic islands of speciation in *Anopheles gambiae*. *PLOS Biology* **3**, e285.
- Turner LM, Harr B.** 2014. Genome-wide mapping in a house mouse hybrid zone reveals hybrid sterility loci and Dobzhansky-Muller interactions. *eLife* **3**, e02504.
- van Wyk AM, Dalton DL, Hoban S, Bruford MW, Russo IM, Birss C, Grobler P, van Vuuren BJ, Kotzé A.** 2017. Quantitative evaluation of hybridization and the impact on biodiversity conservation. *Ecology and Evolution* **7**, 320–330.
- Vernot B, Akey JM.** 2014. Resurrecting surviving Neandertal lineages from modern human genomes. *Science* **343**, 1017–1021.
- Via S.** 2012. Divergence hitchhiking and the spread of genomic isolation during ecological speciation-with-gene-flow. *Philosophical Transactions of the Royal Society B* **367**, 451–460.
- Wang GX, Lv J, Zhang J, Han S, Zong M, Guo N, Zeng XY, Zhang YY, Wang YP, Liu F.** 2016. Genetic and epigenetic alterations of *Brassica nigra* introgression lines from somatic hybridization: a resource for cauliflower improvement. *Frontiers in Plant Science* **7**, 1258.
- Wang H, Vieira FG, Crawford JE, Chu C, Nielsen R.** 2017. Asian wild rice is a hybrid swarm with extensive gene flow and feralization from domesticated rice. *Genome Research* **27**, 1029–1038.
- Ward BJ, van Oosterhout C.** 2016. HYBRIDCHECK: software for the rapid detection, visualization and dating of recombinant regions in genome sequence data. *Molecular Ecology Resources* **16**, 534–539.
- Weill M, Chandre F, Brengues C, Manguin S, Akogbeto M, Pasteur N, Guillet P, Raymond M.** 2000. The *kdr* mutation occurs in the Mopti form of *Anopheles gambiae* s.s. through introgression. *Insect Molecular Biology* **9**, 451–455.
- Wen D, Yu Y, Hahn MW, Nakhleh L.** 2016. Reticulate evolutionary history and extensive introgression in mosquito species revealed by phylogenetic network analysis. *Molecular Ecology* **25**, 2361–2372.
- White BJ, Cheng C, Simard F, Costantini C, Besansky NJ.** 2010. Genetic association of physically unlinked islands of genomic divergence in incipient species of *Anopheles gambiae*. *Molecular Ecology* **19**, 925–939.
- Whitney KD, Broman KW, Kane NC, Hovick SM, Randell RA, Rieseberg LH.** 2015. QTL mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. *Molecular Ecology* **24**, 2194–2211.
- Whitney KD, Randell RA, Rieseberg LH.** 2010. Adaptive introgression of abiotic tolerance traits in the sunflower *Helianthus annuus*. *New Phytologist* **187**, 230–239.
- Wilcox JT, Padgett-Flohr GE, Alvarez JA, Johnson JR.** 2015. Possible phenotypic influence of superinvasive alleles on larval California tiger salamanders (*Ambystoma californiense*). *The American Midland Naturalist* **173**, 168–175.
- Wolf JB, Ellegren H.** 2017. Making sense of genomic islands of differentiation in light of speciation. *Nature reviews. Genetics* **18**, 87–100.
- Wolf DE, Takebayashi N, Rieseberg LH.** 2001. Predicting the risk of extinction through hybridization. *Conservation Biology* **15**, 1039–1053.
- Won H, Renner SS.** 2003. Horizontal gene transfer from flowering plants to *Gnetum*. *Proceedings of the National Academy of Sciences, USA* **100**, 10824–10829.
- Wu CI, Ting CT.** 2004. Genes and speciation. *Nature reviews. Genetics* **5**, 114–122.
- Wybouw N, Pauchet Y, Heckel DG, Van Leeuwen T.** 2016. Horizontal Gene Transfer Contributes to the Evolution of Arthropod Herbivory. *Genome Biology and Evolution* **8**, 1785–1801.
- Xi Z, Bradley RK, Wurdack KJ, Wong K, Sugumaran M, Bomblies K, Rest JS, Davis CC.** 2012. Horizontal transfer of expressed genes in a parasitic flowering plant. *BMC Genomics* **13**, 227.
- Yang Z, Liu L, Fang H, Li P, Xu S, Cao W, Xu C.** 2016. Origin of the plant *Tm-1-like* gene via two independent horizontal transfer events and one gene fusion event. *Scientific Reports* **6**, 33691.
- Yang Z, Wang Y, Zhou Y, Gao Q, Zhang E, Zhu L, Hu Y, Xu C.** 2013. Evolution of land plant genes encoding L-Ala-D/L-Glu epimerases (AEEs) via horizontal gene transfer and positive selection. *BMC Plant Biology* **13**, 34.
- Yang Z, Zhang Y, Wafula EK, et al.** 2016. Horizontal gene transfer is more frequent with increased heterotrophy and contributes to parasite adaptation. *Proceedings of the National Academy of Sciences, USA* **113**, E7010–E7019.
- Yant L, Hollister JD, Wright KM, Arnold BJ, Higgins JD, Franklin FCH, Bomblies K.** 2013. Meiotic adaptation to genome duplication in *Arabidopsis arenosa*. *Current Biology: CB* **23**, 2151–2156.
- Yin Z, Zhu B, Feng H, Huang L.** 2016. Horizontal gene transfer drives adaptive colonization of apple trees by the fungal pathogen *Valsa mali*. *Scientific Reports* **6**, 33129.
- Yoshida S, Maruyama S, Nozaki H, Shirasu K.** 2010. Horizontal gene transfer by the parasitic plant *Striga hermonthica*. *Science* **328**, 1128.
- Yue J, Hu X, Huang J.** 2013. Horizontal gene transfer in the innovation and adaptation of land plants. *Plant Signaling & Behavior* **8**, e24130.
- Yue J, Hu X, Sun H, Yang Y, Huang J.** 2012. Widespread impact of horizontal gene transfer on plant colonization of land. *Nature Communications* **3**, 1152.
- Zalapa JE, Brunet J, Guries RP.** 2009. Patterns of hybridization and introgression between invasive *Ulmus pumila* (Ulmaceae) and native *U. rubra*. *American Journal of Botany* **96**, 1116–1128.
- Zhang W, Dasmahapatra KK, Mallet J, Moreira GR, Kronforst MR.** 2016. Genome-wide introgression among distantly related *Heliconius* butterfly species. *Genome Biology* **17**, 25.
- Zhang Y, Fernandez-Aparicio M, Wafula EK, et al.** 2013. Evolution of a horizontally acquired legume gene, albumin **1**, in the parasitic plant *Phelipanche aegyptiaca* and related species. *BMC Evolutionary Biology* **13**, 48.
- Zhang D, Qi J, Yue J, et al.** 2014. Root parasitic plant *Orobanchae aegyptiaca* and shoot parasitic plant *Cuscuta australis* obtained Brassicaceae-specific *strictosidine synthase-like* genes by horizontal gene transfer. *BMC Plant Biology* **14**, 19.
- Zhu B, Lou MM, Xie GL, Zhang GQ, Zhou XP, Li B, Jin GL.** 2011. Horizontal gene transfer in silkworm, *Bombyx mori*. *BMC Genomics* **12**, 248.
- Zohren J, Wang N, Kardailsky I, Borrell JS, Joecker A, Nichols RA, Buggs RJ.** 2016. Unidirectional diploid-tetraploid introgression among British birch trees with shifting ranges shown by restriction site-associated markers. *Molecular Ecology* **25**, 2413–2426.